

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
Pace, Gary M.
Suttie, Janet L.

(ii) TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

(iii) NUMBER OF SEQUENCES: 94

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Syngenta Biotechnology, Inc.
(B) STREET: 3054 Cornwallis Road
(C) CITY: Research Triangle Park
(D) STATE: NC
(E) COUNTRY: USA
(F) ZIP: 27709

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/547,422
(B) FILING DATE: 11-APR-2000

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/459,504
(B) FILING DATE: 02-JUN-1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/951,715
(B) FILING DATE: 25-SEP-1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/772,027
(B) FILING DATE: 04-OCT-1991

(viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Meigs, J. Timothy
 (B) REGISTRATION NUMBER: 38,241
 (C) REFERENCE/DOCKET NUMBER: S-18805I

(ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: (919)541-8587
 (B) TELEFAX: (919)541-8689

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3468 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus thuringiensis kurstaki*
 (B) STRAIN: HD-1

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..3468
 (D) OTHER INFORMATION: /product= "Full-length native
 cryIA(b)"
 /note= "Appears in Figures 1 and 4 as BTHKURHD."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GTTGATATAA TATGGGGAAT TTTTGGTCCC TCTCAATGGG ACGCATTCT TGTACAAATT	240
GAACAGTTAA TTAACCAAAG AATAGAAGAA TTCGCTAGGA ACCAAGCCAT TTCTAGATTA	300
GAAGGACTAA GCAATCTTTA TCAAATTTAC GCAGAATCTT TTAGAGAGTG GGAAGCAGAT	360
CCTACTAATC CAGCATTAAAG AGAAGAGATG CGTATTCAAT TCAATGACAT GAACAGTGCC	420
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AGGTGGGGAT TTGATGCCGC GACTATCAAT AGTCGTTATA ATGATTTAAC TAGGCTTATT	600
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CCGGATTCTA GAGATTGGAT AAGATATAAT CAATTTAGAA GAGAATTAAC ACTAACTGTA	720
TTAGATATCG TTTCTCTATT TCCGAACAT GATAGTAGAA CGTATCCAAT TCGAACAGTT	780

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ATAATGGCTT CTCCTGTAGG GTTTTCGGGG CCAGAATTCA CTTTTCGCT ATATGGAAC	1020
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GCGATGATTC ATGCGGCAGA TAAACGCGTT CATAGCATTC GAGAAGCTTA TCTGCCTGAG      2760
CTGTCTGTGA TTCCGGGTGT CAATGCGGCT ATTTTGAAG AATTAGAAGG GCGTATTTTC      2820
ACTGCATTCT CCCTATATGA TGCGAGAAAT GTCATTAAAA ATGGTGATTT TAATAATGGC      2880
TTATCCTGCT GGAACGTGAA AGGGCATGTA GATGTAGAAG AACAAAACAA CCACCGTTCG      2940
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CGTGGCTATA TCCTTCGTGT CACAGCGTAC AAGGAGGGAT ATGGAGAAGG TTGCGTAACC      3060
ATTCATGAGA TCGAGAACAA TACAGACGAA CTGAAGTTTA GCAACTGTGT AGAAGAGGAA      3120
GTATATCCAA ACAACACGGT AACGTGTAAT GATTATACTG CGACTCAAGA AGAATATGAG      3180
GGTACGTACA CTTCTCGTAA TCGAGGATAT GACGGAGCCT ATGAAAGCAA TTCTTCTGTA      3240
CCAGCTGATT ATGCATCAGC CTATGAAGAA AAAGCATATA CAGATGGACG AAGAGACAAT      3300
CCTTGTGAAT CTAACAGAGG ATATGGGGAT TACACACCAC TACCAGCTGG CTATGTGACA      3360
AAAGAATTAG AGTACTTCCC AGAAACCGAT AAGGTATGGA TTGAGATCGG AGAAACGGAA      3420
GGAACATTCA TCGTGGACAG CGTGGGAATTA CTTCTTATGG AGGAATAA      3468

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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..3468
 - (D) OTHER INFORMATION: /product= "Full-length pure maize optimized synthetic Bt"
 - /note= "Disclosed in Figure 3 as syn1T.mze"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1947 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..1947
 (D) OTHER INFORMATION: /product= "Truncated synthetic
 maize optimized cryIA(b) gene"
 /note= "Disclosed in Figures 1, 2, 3, 4 and 5 as bssyn."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..3468
 - (D) OTHER INFORMATION: /product= "Full length synthetic maize optimized"
- /note= "Disclosed in Figure 3 as synful.mod. This sequence is identical to flsynbt.fin as disclosed in Figure 1."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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CGCGGCAGCG	CCCAGGGCAT	CGAGGGCAGC	ATCCGCAGCC	CCCACCTGAT	GGACATCCTG	900
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TACCGCAAGA	GCGGCACCGT	GGACAGCCTG	GACGAGATCC	CCCCTCAGAA	CAACAACGTG	1260
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GAGTTCAACA	ACATCATCCC	CAGCAGCCAG	ATCACCCAGA	TCCCCCTGAC	CAAGAGCACC	1440
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CTGCAGAGCG	GCAGCTTCCG	CACCGTGGGC	TTCACCACCC	CCTTCAACTT	CAGCAACGGC	1740
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CACTTCAGCC	TGGACATCGA	CGTGGGCTGC	ACCGACCTGA	ACGAGGACCT	GGGCGTGTGG	2460

GTTGAAGTAC	TTGGTGGAGA	ACGCATTGAA	ACCGGTTACA	CTCCCATCGA	CATCTCCTTG	120
TCCTTGACAC	AGTTTCTGCT	CAGCGAGTTC	GTGCCAGGTG	CTGGGTTCGT	TCTCGGACTA	180
GTTGACATCA	TCTGGGGTAT	CTTTGGTCCA	TCTCAATGGG	ATGCATTCTT	GGTGCAAATT	240
GAGCAGTTGA	TCAACCAGAG	GATCGAAGAG	TTCGCCAGGA	ACCAGGCCAT	CTCTAGGTTG	300
GAAGGATTGA	GCAATCTCTA	CCAAATCTAT	GCAGAGAGCT	TCAGAGAGTG	GGAAGCCGAT	360
CCTACTAACC	CAGCTCTCCG	CGAGGAAATG	CGTATTCAAT	TCAACGACAT	GAACAGCGCC	420
TTGACCACAG	CTATCCCATT	GTTTCGCAGTC	CAGAACTACC	AAGTTCCTCT	CTTGTCCGTG	480
TACGTTCAAG	CAGCTAATCT	TCACCTCAGC	GTGCTTCGAG	ACGTTAGCGT	GTTTGGGCAA	540
AGGTGGGGAT	TCGATGCTGC	AACCATCAAT	AGCCGTTACA	ACGACCTTAC	TAGGCTGATT	600
GGAAACTACA	CCGACCACGC	TGTTTCGTTGG	TACAACACTG	GCTTGGAGCG	TGTCTGGGGT	660
CCTGATTCTA	GAGATTGGAT	TAGATACAAC	CAGTTCAGGA	GAGAATTGAC	CCTCACAGTT	720
TTGGACATTG	TGTCTCTCTT	CCCGAACTAT	GACTCCAGAA	CCTACCCTAT	CCGTACAGTG	780
TCCCAACTTA	CCAGAGAAAT	CTATACTAAC	CCAGTTCTTG	AGAACTTCGA	CGGTAGCTTC	840
CGTGGTTCTG	CCCAAGGTAT	CGAAGGCTCC	ATCAGGAGCC	CACACTTGAT	GGACATCTTG	900
AACAGCATAA	CTATCTACAG	CGATGCTCAC	AGAGGAGAGT	ATTACTGGTC	TGGACACCAG	960
ATCATGGCCT	CTCCAGTTGG	ATTCAGCGGG	CCCGAGTTTA	CCTTTCCTCT	CTATGGAAct	1020
ATGGGAAACG	CCGCTCCACA	ACAACGTATC	GTGCTCAAC	TAGGTCAGGG	TGTCTACAGA	1080
ACCTTGTCTT	CCACCTTGTA	CAGAAGACCC	TTCAATATCG	GTATCAACAA	CCAGCAACTT	1140
TCCGTTCTTG	ACGGAACAGA	GTTTCGCCTAT	GGAACCTCTT	CTAACTTGCC	ATCCGCTGTT	1200
TACAGAAAGA	GCGGAACCGT	TGATTCTCTG	GACGAAATCC	CACCACAGAA	CAACAATGTG	1260
CCACCCAGGC	AAGGATTCTC	CCACAGGTTG	AGCCACGTGT	CCATGTTCCG	TTCCGGATTG	1320
AGCAACAGTT	CCGTGAGCAT	CATCAGAGCT	CCTATGTTCT	CATGGATTCA	TCGTAGTGCT	1380
GAGTTCAACA	ATATCATTCC	TTCCTCTCAA	ATCACCCAAA	TCCCATTGAC	CAAGTCTACT	1440
AACCTTGGAT	CTGGAACCTT	TGTCGTGAAA	GGACCAGGCT	TCACAGGAGG	TGATATTCTT	1500
AGAAGAACTT	CTCCTGGCCA	GATTAGCACC	CTCAGAGTTA	ACATCACTGC	ACCACTTTCT	1560
CAAAGATATC	GTGTCAGGAT	TCGTTACGCA	TCTACCACTA	ACTTGCAATT	CCACACCTCC	1620
ATCGACGGAA	GGCCTATCAA	TCAGGGTAAC	TTCTCCGCAA	CCATGTCAAG	CGGCAGCAAC	1680
TTGCAATCCG	GCAGCTTCAG	AACCGTCGGT	TTCCTACTCT	CTTTCAACTT	CTCTAACGGA	1740
TCAAGCGTTT	TCACCCTTAG	CGCTCATGTG	TTCAATTCTG	GCAATGAAGT	GTACATTGAC	1800
CGTATTGAGT	TTGTGCCTGC	CGAAGTTACC	TTGAGGCTG	AGTAC		1845

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3624 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..3621
 (D) OTHER INFORMATION: /product= "Full-length, maize
 optimized cryIB"
 /note= "Disclosed in Figure 6."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG GAC CTG CTG CCC GAC GCC CGC ATC GAG GAC AGC CTG TGC ATC GCC	48
Met Asp Leu Leu Pro Asp Ala Arg Ile Glu Asp Ser Leu Cys Ile Ala	
1 5 10 15	
GAG GGC AAC AAC ATC GAC CCC TTC GTG AGC GCC AGC ACC GTG CAG ACC	96
Glu Gly Asn Asn Ile Asp Pro Phe Val Ser Ala Ser Thr Val Gln Thr	
20 25 30	
GGC ATC AAC ATC GCC GGC CGC ATC CTG GGC GTG CTG GGC GTG CCC TTC	144
Gly Ile Asn Ile Ala Gly Arg Ile Leu Gly Val Leu Gly Val Pro Phe	
35 40 45	
GCC GGC CAG CTG GCC AGC TTC TAC AGC TTC CTG GTG GGC GAG CTG TGG	192
Ala Gly Gln Leu Ala Ser Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp	
50 55 60	
CCC CGC GGC CGC GAC CAG TGG GAG ATC TTC CTG GAG CAC GTG GAG CAG	240
Pro Arg Gly Arg Asp Gln Trp Glu Ile Phe Leu Glu His Val Glu Gln	
65 70 75 80	
CTG ATC AAC CAG CAG ATC ACC GAG AAC GCC CGC AAC ACC GCC CTG GCC	288
Leu Ile Asn Gln Gln Ile Thr Glu Asn Ala Arg Asn Thr Ala Leu Ala	
85 90 95	
CGC CTG CAG GGC CTG GGC GAC AGC TTC CGC GCC TAC CAG CAG AGC CTG	336
Arg Leu Gln Gly Leu Gly Asp Ser Phe Arg Ala Tyr Gln Gln Ser Leu	
100 105 110	
GAG GAC TGG CTG GAG AAC CGC GAC GAC GCC CGC ACC CGC AGC GTG CTG	384
Glu Asp Trp Leu Glu Asn Arg Asp Asp Ala Arg Thr Arg Ser Val Leu	
115 120 125	
TAC ACC CAG TAC ATC GCC CTG GAG CTG GAC TTC CTG AAC GCC ATG CCC	432
Tyr Thr Gln Tyr Ile Ala Leu Glu Leu Asp Phe Leu Asn Ala Met Pro	
130 135 140	
CTG TTC GCC ATC CGC AAC CAG GAG GTG CCC CTG CTG ATG GTG TAC GCC	480
Leu Phe Ala Ile Arg Asn Gln Glu Val Pro Leu Leu Met Val Tyr Ala	

145					150					155					160	
CAG	GCC	GCC	AAC	CTG	CAC	CTG	CTG	CTG	CTG	CGC	GAC	GCC	AGC	CTG	TTC	528
Gln	Ala	Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Arg	Asp	Ala	Ser	Leu	Phe	
				165					170					175		
GGC	AGC	GAG	TTC	GGC	CTG	ACC	AGC	CAG	GAG	ATC	CAG	CGC	TAC	TAC	GAG	576
Gly	Ser	Glu	Phe	Gly	Leu	Thr	Ser	Gln	Glu	Ile	Gln	Arg	Tyr	Tyr	Glu	
			180					185					190			
CGC	CAG	GTG	GAG	CGC	ACC	CGC	GAC	TAC	AGC	GAC	TAC	TGC	GTG	GAG	TGG	624
Arg	Gln	Val	Glu	Arg	Thr	Arg	Asp	Tyr	Ser	Asp	Tyr	Cys	Val	Glu	Trp	
		195					200					205				
TAC	AAC	ACC	GGC	CTG	AAC	AGC	CTG	CGC	GGC	ACC	AAC	GCC	GCC	AGC	TGG	672
Tyr	Asn	Thr	Gly	Leu	Asn	Ser	Leu	Arg	Gly	Thr	Asn	Ala	Ala	Ser	Trp	
	210					215					220					
GTG	CGC	TAC	AAC	CAG	TTC	CGC	CGC	GAC	CTG	ACC	CTG	GGC	GTG	CTG	GAC	720
Val	Arg	Tyr	Asn	Gln	Phe	Arg	Arg	Asp	Leu	Thr	Leu	Gly	Val	Leu	Asp	
225				230				235							240	
CTG	GTG	GCC	CTG	TTC	CCC	AGC	TAC	GAC	ACC	CGC	ACC	TAC	CCC	ATC	AAC	768
Leu	Val	Ala	Leu	Phe	Pro	Ser	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Ile	Asn	
				245				250						255		
ACC	AGC	GCC	CAG	CTG	ACC	CGC	GAG	GTG	TAC	ACC	GAC	GCC	ATC	GGC	GCC	816
Thr	Ser	Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Ala	Ile	Gly	Ala	
			260					265					270			
ACC	GGC	GTG	AAC	ATG	GCC	AGC	ATG	AAC	TGG	TAC	AAC	AAC	AAC	GCC	CCC	864
Thr	Gly	Val	Asn	Met	Ala	Ser	Met	Asn	Trp	Tyr	Asn	Asn	Asn	Ala	Pro	
		275					280					285				
AGC	TTC	AGC	GCC	ATC	GAG	GCC	GCC	GCC	ATC	CGC	AGC	CCC	CAC	CTG	CTG	912
Ser	Phe	Ser	Ala	Ile	Glu	Ala	Ala	Ala	Ile	Arg	Ser	Pro	His	Leu	Leu	
	290					295					300					
GAC	TTC	CTG	GAG	CAG	CTG	ACC	ATC	TTC	AGC	GCC	AGC	AGC	CGC	TGG	AGC	960
Asp	Phe	Leu	Glu	Gln	Leu	Thr	Ile	Phe	Ser	Ala	Ser	Ser	Arg	Trp	Ser	
305				310				315						320		
AAC	ACC	CGC	CAC	ATG	ACC	TAC	TGG	CGC	GGC	CAC	ACC	ATC	CAG	AGC	CGC	1008
Asn	Thr	Arg	His	Met	Thr	Tyr	Trp	Arg	Gly	His	Thr	Ile	Gln	Ser	Arg	
				325				330						335		
CCC	ATC	GGC	GGC	GGC	CTG	AAC	ACC	AGC	ACC	CAC	GGC	GCC	ACC	AAC	ACC	1056
Pro	Ile	Gly	Gly	Gly	Leu	Asn	Thr	Ser	Thr	His	Gly	Ala	Thr	Asn	Thr	
			340					345				350				
AGC	ATC	AAC	CCC	GTG	ACC	CTG	CGC	TTC	GCC	AGC	CGC	GAC	GTG	TAC	CGC	1104
Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Phe	Ala	Ser	Arg	Asp	Val	Tyr	Arg	
		355					360					365				
ACC	GAG	AGC	TAC	GCC	GGC	GTG	CTG	CTG	TGG	GGC	ATC	TAC	CTG	GAG	CCC	1152
Thr	Glu	Ser	Tyr	Ala	Gly	Val	Leu	Leu	Trp	Gly	Ile	Tyr	Leu	Glu	Pro	
	370					375					380					
ATC	CAC	GGC	GTG	CCC	ACC	GTG	CGC	TTC	AAC	TTC	ACC	AAC	CCC	CAG	AAC	1200
Ile	His	Gly	Val	Pro	Thr	Val	Arg	Phe	Asn	Phe	Thr	Asn	Pro	Gln	Asn	
385				390					395					400		

ATC AGC GAC CGC GGC ACC GCC AAC TAC AGC CAG CCC TAC GAG AGC CCC	1243
Ile Ser Asp Arg Gly Thr Ala Asn Tyr Ser Gln Pro Tyr Glu Ser Pro	
405 410 415	
GGC CTG CAG CTG AAG GAC AGC GAG ACC GAG CTG CCC CCC GAG ACC ACC	1295
Gly Leu Gln Leu Lys Asp Ser Glu Thr Glu Leu Pro Pro Glu Thr Thr	
420 425 430	
GAG CGC CCC AAC TAC GAG AGC TAC AGC CAC CGC CTG AGC CAC ATC GGC	1344
Glu Arg Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly	
435 440 445	
ATC ATC CTG CAG AGC CGC GTG AAC GTG CCC GTG TAC AGC TGG ACC CAC	1392
Ile Ile Leu Gln Ser Arg Val Asn Val Pro Val Tyr Ser Trp Thr His	
450 455 460	
CGC AGC GCC GAC CGC ACC AAC ACC ATC GGC CCC AAC CGC ATC ACC CAG	1440
Arg Ser Ala Asp Arg Thr Asn Thr Ile Gly Pro Asn Arg Ile Thr Gln	
465 470 475 480	
ATC CCC ATG GTG AAG GCC AGC GAG CTG CCC CAG GGC ACC ACC GTG GTG	1483
Ile Pro Met Val Lys Ala Ser Glu Leu Pro Gln Gly Thr Thr Val Val	
485 490 495	
CGC GGC CCC GGC TTC ACC GGC GGC GAC ATC CTG CGC CGC ACC AAC ACC	1536
Arg Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr	
500 505 510	
GGC GGC TTC GGC CCC ATC CGC GTG ACC GTG AAC GGC CCC CTG ACC CAG	1584
Gly Gly Phe Gly Pro Ile Arg Val Thr Val Asn Gly Pro Leu Thr Gln	
515 520 525	
CGC TAC CGC ATC GGC TTC CGC TAC GCC AGC ACC GTG GAC TTC GAC TTC	1632
Arg Tyr Arg Ile Gly Phe Arg Tyr Ala Ser Thr Val Asp Phe Asp Phe	
530 535 540	
TTC GTG AGC CGC GGC GGC ACC ACC GTG AAC AAC TTC CGC TTC CTG CGC	1680
Phe Val Ser Arg Gly Gly Thr Thr Val Asn Asn Phe Arg Phe Leu Arg	
545 550 555 560	
ACC ATG AAC AGC GGC GAC GAG CTG AAG TAC GGC AAC TTC GTG CGC CGC	1728
Thr Met Asn Ser Gly Asp Glu Leu Lys Tyr Gly Asn Phe Val Arg Arg	
565 570 575	
GCC TTC ACC ACC CCC TTC ACC TTC ACC CAG ATC CAG GAC ATC ATC CGC	1776
Ala Phe Thr Thr Pro Phe Thr Phe Thr Gln Ile Gln Asp Ile Ile Arg	
580 585 590	
ACC AGC ATC CAG GGC CTG AGC GGC AAC GGC GAG GTG TAC ATC GAC AAG	1824
Thr Ser Ile Gln Gly Leu Ser Gly Asn Gly Glu Val Tyr Ile Asp Lys	
595 600 605	
ATC GAG ATC ATC CCC GTG ACC GCC ACC TTC GAG GCC GAG TAC GAC CTG	1872
Ile Glu Ile Ile Pro Val Thr Ala Thr Phe Glu Ala Glu Tyr Asp Leu	
610 615 620	
GAG CGC GCC CAG GAG GCC GTG AAC GCC CTG TTC ACC AAC ACC AAC CCC	1920
Glu Arg Ala Gln Glu Ala Val Asn Ala Leu Phe Thr Asn Thr Asn Pro	
625 630 635 640	

CGC	CGC	CTG	AAG	ACC	GAC	GTG	ACC	GAC	TAC	CAC	ATC	GAC	CAG	GTG	AGC	1963
Arg	Arg	Leu	Lys	Thr	Asp	Val	Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	
				645					650					655		
AAC	CTG	GTG	GCC	TGC	CTG	AGC	GAC	GAG	TTC	TGC	CTG	GAC	GAG	AAG	CGC	2015
Asn	Leu	Val	Ala	Cys	Leu	Ser	Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Arg	
			660					665					670			
GAG	CTG	CTG	GAG	AAG	GTG	AAG	TAC	GCC	AAG	CGC	CTG	AGC	GAC	GAG	CGC	2064
Glu	Leu	Leu	Glu	Lys	Val	Lys	Tyr	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	
			675				680					685				
AAC	CTG	CTG	CAG	GAC	CCC	AAC	TTC	ACC	AGC	ATC	AAC	AAG	CAG	CCC	GAC	2112
Asn	Leu	Leu	Gln	Asp	Pro	Asn	Phe	Thr	Ser	Ile	Asn	Lys	Gln	Pro	Asp	
	690					695					700					
TTC	ATC	AGC	ACC	AAC	GAG	CAG	AGC	AAC	TTC	ACC	AGC	ATC	CAC	GAG	CAG	2163
Phe	Ile	Ser	Thr	Asn	Glu	Gln	Ser	Asn	Phe	Thr	Ser	Ile	His	Glu	Gln	
705					710					715					720	
AGC	GAG	CAC	GGC	TGG	TGG	GGC	AGC	GAG	AAC	ATC	ACC	ATC	CAG	GAG	GGC	2208
Ser	Glu	His	Gly	Trp	Trp	Gly	Ser	Glu	Asn	Ile	Thr	Ile	Gln	Glu	Gly	
				725					730					735		
AAC	GAC	GTG	TTC	AAG	GAG	AAC	TAC	GTG	ACC	CTG	CCC	GGC	ACC	TTC	AAC	2256
Asn	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	Thr	Leu	Pro	Gly	Thr	Phe	Asn	
			740					745					750			
GAG	TGC	TAC	CCC	ACC	TAC	CTG	TAC	CAG	AAG	ATC	GGC	GAG	AGC	GAG	CTG	2304
Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	Lys	Ile	Gly	Glu	Ser	Glu	Leu	
			755				760					765				
AAG	GCC	TAC	ACC	CGC	TAC	CAG	CTG	CGC	GGC	TAC	ATC	GAG	GAC	AGC	CAG	2352
Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg	Gly	Tyr	Ile	Glu	Asp	Ser	Gln	
	770					775					780					
GAC	CTG	GAG	ATC	TAC	CTG	ATC	CGC	TAC	AAC	GCC	AAG	CAC	GAG	ACC	CTG	2400
Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	Asn	Ala	Lys	His	Glu	Thr	Leu	
	785				790					795					800	
GAC	GTG	CCC	GGC	ACC	GAG	AGC	CTG	TGG	CCC	CTG	AGC	GTG	GAG	AGC	CCC	2448
Asp	Val	Pro	Gly	Thr	Glu	Ser	Leu	Trp	Pro	Leu	Ser	Val	Glu	Ser	Pro	
				805					810					815		
ATC	GGC	CGC	TGC	GGC	GAG	CCC	AAC	CGC	TGC	GCC	CCC	CAC	TTC	GAG	TGG	2496
Ile	Gly	Arg	Cys	Gly	Glu	Pro	Asn	Arg	Cys	Ala	Pro	His	Phe	Glu	Trp	
			820					825					830			
AAC	CCC	GAC	CTG	GAC	TGC	AGC	TGC	CGC	GAC	GGC	GAG	AAG	TGC	GCC	CAC	2544
Asn	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg	Asp	Gly	Glu	Lys	Cys	Ala	His	
			835				840					845				
CAC	AGC	CAC	CAC	TTC	AGC	CTG	GAC	ATC	GAC	GTG	GGC	TGC	ACC	GAC	CTG	2592
His	Ser	His	His	Phe	Ser	Leu	Asp	Ile	Asp	Val	Gly	Cys	Thr	Asp	Leu	
	850					855					860					
CAC	GAG	AAC	CTG	GGC	GTG	TGG	GTG	GTG	TTC	AAG	ATC	AAG	ACC	CAG	GAG	2640
His	Glu	Asn	Leu	Gly	Val	Trp	Val	Val	Phe	Lys	Ile	Lys	Thr	Gln	Glu	
	865				870					875					880	
GGC	CAC	GCC	CGC	CTG	GGC	AAC	CTG	GAG	TTC	ATC	GAG	GAG	AAG	CCC	CTG	2688

Gly	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu	Phe	Ile	Glu	Glu	Lys	Pro	Leu		
				885					890					895			
CTG	GGC	GAG	GCC	CTG	AGC	CGC	GTG	AAG	CGC	GCC	GAG	AAG	AAG	TGG	CGC		2736
Leu	Gly	Glu	Ala	Leu	Ser	Arg	Val	Lys	Arg	Ala	Glu	Lys	Lys	Trp	Arg		
			900					905					910				
GAC	AAG	CGC	GAG	AAG	CTG	CAG	CTG	GAG	ACC	AAG	CGC	GTG	TAC	ACC	GAG		2784
Asp	Lys	Arg	Glu	Lys	Leu	Gln	Leu	Glu	Thr	Lys	Arg	Val	Tyr	Thr	Glu		
		915					920					925					
GCC	AAG	GAG	GCC	GTG	GAC	GCC	CTG	TTC	GTG	GAC	AGC	CAG	TAC	GAC	CGC		2832
Ala	Lys	Glu	Ala	Val	Asp	Ala	Leu	Phe	Val	Asp	Ser	Gln	Tyr	Asp	Arg		
	930					935					940						
CTG	CAG	GCC	GAC	ACC	AAC	ATC	GGC	ATG	ATC	CAC	GCC	GCC	GAC	AAG	CTG		2880
Leu	Gln	Ala	Asp	Thr	Asn	Ile	Gly	Met	Ile	His	Ala	Ala	Asp	Lys	Leu		
945					950					955					960		
GTG	CAC	CGC	ATC	CGC	GAG	GCC	TAC	CTG	AGC	GAG	CTG	CCC	GTG	ATC	CCC		2928
Val	His	Arg	Ile	Arg	Glu	Ala	Tyr	Leu	Ser	Glu	Leu	Pro	Val	Ile	Pro		
			965					970					975				
GGC	GTG	AAC	GCC	GAG	ATC	TTC	GAG	GAG	CTG	GAG	GGC	CAC	ATC	ATC	ACC		2976
Gly	Val	Asn	Ala	Glu	Ile	Phe	Glu	Glu	Leu	Glu	Gly	His	Ile	Ile	Thr		
			980				985					990					
GCC	ATC	AGC	CTG	TAC	GAC	GCC	CGC	AAC	GTG	GTG	AAG	AAC	GGC	GAC	TTC		3024
Ala	Ile	Ser	Leu	Tyr	Asp	Ala	Arg	Asn	Val	Val	Lys	Asn	Gly	Asp	Phe		
		995					1000					1005					
AAC	AAC	GGC	CTG	ACC	TGC	TGG	AAC	GTG	AAG	GGC	CAC	GTG	GAC	GTG	CAG		3072
Asn	Asn	Gly	Leu	Thr	Cys	Trp	Asn	Val	Lys	Gly	His	Val	Asp	Val	Gln		
	1010					1015					1020						
CAG	AGC	CAC	CAC	CGC	AGC	GAC	CTG	GTG	ATC	CCC	GAG	TGG	GAG	GCC	GAG		3120
Gln	Ser	His	His	Arg	Ser	Asp	Leu	Val	Ile	Pro	Glu	Trp	Glu	Ala	Glu		
1025				1030						1035					1040		
GTG	AGC	CAG	GCC	GTG	CGC	GTG	TGC	CCC	GGC	TGC	GGC	TAC	ATC	CTG	CGC		3168
Val	Ser	Gln	Ala	Val	Arg	Val	Cys	Pro	Gly	Cys	Gly	Tyr	Ile	Leu	Arg		
			1045					1050					1055				
GTG	ACC	GCC	TAC	AAG	GAG	GGC	TAC	GGC	GAG	GGC	TGC	GTG	ACC	ATC	CAC		3216
Val	Thr	Ala	Tyr	Lys	Glu	Gly	Tyr	Gly	Glu	Gly	Cys	Val	Thr	Ile	His		
			1060				1065					1070					
GAG	ATC	GAG	AAC	AAC	ACC	GAC	GAG	CTG	AAG	TTC	AAG	AAC	CGC	GAG	GAG		3264
Glu	Ile	Glu	Asn	Asn	Thr	Asp	Glu	Leu	Lys	Phe	Lys	Asn	Arg	Glu	Glu		
		1075					1080				1085						
GAG	GAG	GTG	TAC	CCC	ACC	GAC	ACC	GGC	ACC	TGC	AAC	GAC	TAC	ACC	GCC		3312
Glu	Glu	Val	Tyr	Pro	Thr	Asp	Thr	Gly	Thr	Cys	Asn	Asp	Tyr	Thr	Ala		
	1090					1095					1100						
CAC	CAG	GGC	ACC	GCC	GGC	TGC	GCC	GAC	GCC	TGC	AAC	AGC	CGC	AAC	GCC		3360
His	Gln	Gly	Thr	Ala	Gly	Cys	Ala	Asp	Ala	Cys	Asn	Ser	Arg	Asn	Ala		
1105				1110						1115					1120		
GGC	TAC	GAG	GAC	GCC	TAC	GAG	GTG	GAC	ACC	ACC	GCC	AGC	GTG	AAC	TAC		3408
Gly	Tyr	Glu	Asp	Ala	Tyr	Glu	Val	Asp	Thr	Thr	Ala	Ser	Val	Asn	Tyr		

	1125	1130	1135	
AAG CCC ACC TAC GAG GAG GAG ACC TAC ACC GAC GTG CGC CGC GAC AAC				3456
Lys Pro Thr Tyr Glu Glu Glu Thr Tyr Thr Asp Val Arg Arg Asp Asn				
	1140	1145	1150	
CAC TGC GAG TAC GAC CGC GGC TAC GTG AAC TAC CCC CCC GTG CCC GCC				3504
His Cys Glu Tyr Asp Arg Gly Tyr Val Asn Tyr Pro Pro Val Pro Ala				
	1155	1160	1165	
GGC TAC GTG ACC AAG GAG CTG GAG TAC TTC CCC GAG ACC GAC ACC GTG				3552
Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Thr Val				
	1170	1175	1180	
TGG ATC GAG ATC GGC GAG ACC GAG GGC AAG TTC ATC GTG GAC AGC GTG				3600
Trp Ile Glu Ile Gly Glu Thr Glu Gly Lys Phe Ile Val Asp Ser Val				
	1185	1190	1195	1200
GAG CTG CTG CTG ATG GAG GAG TAG				3624
Glu Leu Leu Leu Met Glu Glu				
	1205			

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1207 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Asp	Leu	Leu	Pro	Asp	Ala	Arg	Ile	Glu	Asp	Ser	Leu	Cys	Ile	Ala
1				5					10					15	
Glu	Gly	Asn	Asn	Ile	Asp	Pro	Phe	Val	Ser	Ala	Ser	Thr	Val	Gln	Thr
		20						25					30		
Gly	Ile	Asn	Ile	Ala	Gly	Arg	Ile	Leu	Gly	Val	Leu	Gly	Val	Pro	Phe
		35					40					45			
Ala	Gly	Gln	Leu	Ala	Ser	Phe	Tyr	Ser	Phe	Leu	Val	Gly	Glu	Leu	Trp
	50					55					60				
Pro	Arg	Gly	Arg	Asp	Gln	Trp	Glu	Ile	Phe	Leu	Glu	His	Val	Glu	Gln
	65				70					75				80	
Leu	Ile	Asn	Gln	Gln	Ile	Thr	Glu	Asn	Ala	Arg	Asn	Thr	Ala	Leu	Ala
			85						90					95	
Arg	Leu	Gln	Gly	Leu	Gly	Asp	Ser	Phe	Arg	Ala	Tyr	Gln	Gln	Ser	Leu
		100						105					110		
Glu	Asp	Trp	Leu	Glu	Asn	Arg	Asp	Asp	Ala	Arg	Thr	Arg	Ser	Val	Leu
	115						120				125				
Tyr	Thr	Gln	Tyr	Ile	Ala	Leu	Glu	Leu	Asp	Phe	Leu	Asn	Ala	Met	Pro
	130					135						140			

Leu Phe Ala Ile Arg Asn Gln Glu Val Pro Leu Leu Met Val Tyr Ala
 145 150 155 160
 Gln Ala Ala Asn Leu His Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe
 165 170 175
 Gly Ser Glu Phe Gly Leu Thr Ser Gln Glu Ile Gln Arg Tyr Tyr Glu
 180 185 190
 Arg Gln Val Glu Arg Thr Arg Asp Tyr Ser Asp Tyr Cys Val Glu Trp
 195 200 205
 Tyr Asn Thr Gly Leu Asn Ser Leu Arg Gly Thr Asn Ala Ala Ser Trp
 210 215 220
 Val Arg Tyr Asn Gln Phe Arg Arg Asp Leu Thr Leu Gly Val Leu Asp
 225 230 235 240
 Leu Val Ala Leu Phe Pro Ser Tyr Asp Thr Arg Thr Tyr Pro Ile Asn
 245 250 255
 Thr Ser Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Ala
 260 265 270
 Thr Gly Val Asn Met Ala Ser Met Asn Trp Tyr Asn Asn Asn Ala Pro
 275 280 285
 Ser Phe Ser Ala Ile Glu Ala Ala Ala Ile Arg Ser Pro His Leu Leu
 290 295 300
 Asp Phe Leu Glu Gln Leu Thr Ile Phe Ser Ala Ser Ser Arg Trp Ser
 305 310 315 320
 Asn Thr Arg His Met Thr Tyr Trp Arg Gly His Thr Ile Gln Ser Arg
 325 330 335
 Pro Ile Gly Gly Gly Leu Asn Thr Ser Thr His Gly Ala Thr Asn Thr
 340 345 350
 Ser Ile Asn Pro Val Thr Leu Arg Phe Ala Ser Arg Asp Val Tyr Arg
 355 360 365
 Thr Glu Ser Tyr Ala Gly Val Leu Leu Trp Gly Ile Tyr Leu Glu Pro
 370 375 380
 Ile His Gly Val Pro Thr Val Arg Phe Asn Phe Thr Asn Pro Gln Asn
 385 390 395 400
 Ile Ser Asp Arg Gly Thr Ala Asn Tyr Ser Gln Pro Tyr Glu Ser Pro
 405 410 415
 Gly Leu Gln Leu Lys Asp Ser Glu Thr Glu Leu Pro Pro Glu Thr Thr
 420 425 430
 Glu Arg Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly
 435 440 445
 Ile Ile Leu Gln Ser Arg Val Asn Val Pro Val Tyr Ser Trp Thr His
 450 455 460
 Arg Ser Ala Asp Arg Thr Asn Thr Ile Gly Pro Asn Arg Ile Thr Gln

465		470		475		480
Ile Pro Met Val	Lys Ala Ser Glu Leu	Pro Gln Gly Thr Thr	Val Val			
	485	490	495			
Arg Gly Pro Gly	Phe Thr Gly Gly	Asp Ile Leu Arg Arg	Thr Asn Thr			
	500	505	510			
Gly Gly Phe Gly	Pro Ile Arg Val	Thr Val Asn Gly	Pro Leu Thr Gln			
	515	520	525			
Arg Tyr Arg Ile	Gly Phe Arg Tyr	Ala Ser Thr Val	Asp Phe Asp Phe			
	530	535	540			
Phe Val Ser Arg	Gly Gly Thr Thr	Val Asn Asn Phe	Arg Phe Leu Arg			
	545	550	555			560
Thr Met Asn Ser	Gly Asp Glu Leu	Lys Tyr Gly Asn	Phe Val Arg Arg			
	565	570	575			
Ala Phe Thr Thr	Pro Phe Thr Phe	Thr Gln Ile Gln	Asp Ile Ile Arg			
	580	585	590			
Thr Ser Ile Gln	Gly Leu Ser Gly	Asn Gly Glu Val	Tyr Ile Asp Lys			
	595	600	605			
Ile Glu Ile Ile	Pro Val Thr Ala	Thr Phe Glu Ala	Glu Tyr Asp Leu			
	610	615	620			
Glu Arg Ala Gln	Glu Ala Val Asn	Ala Leu Phe Thr	Asn Thr Asn Pro			
	625	630	635			640
Arg Arg Leu Lys	Thr Asp Val Thr	Asp Tyr His Ile	Asp Gln Val Ser			
	645	650	655			
Asn Leu Val Ala	Cys Leu Ser Asp	Glu Phe Cys Leu	Asp Glu Lys Arg			
	660	665	670			
Glu Leu Leu Glu	Lys Val Lys Tyr	Ala Lys Arg Leu	Ser Asp Glu Arg			
	675	680	685			
Asn Leu Leu Gln	Asp Pro Asn Phe	Thr Ser Ile Asn	Lys Gln Pro Asp			
	690	695	700			
Phe Ile Ser Thr	Asn Glu Gln Ser	Asn Phe Thr Ser	Ile His Glu Gln			
	705	710	715			720
Ser Glu His Gly	Trp Trp Gly Ser	Glu Asn Ile Thr	Ile Gln Glu Gly			
	725	730	735			
Asn Asp Val Phe	Lys Glu Asn Tyr	Val Thr Leu Pro	Gly Thr Phe Asn			
	740	745	750			
Glu Cys Tyr Pro	Thr Tyr Leu Tyr	Gln Lys Ile Gly	Glu Ser Glu Leu			
	755	760	765			
Lys Ala Tyr Thr	Arg Tyr Gln Leu	Arg Gly Tyr Ile	Glu Asp Ser Gln			
	770	775	780			
Asp Leu Glu Ile	Tyr Leu Ile Arg	Tyr Asn Ala Lys	His Glu Thr Leu			
	785	790	795			800

Asp	Val	Pro	Gly	Thr	Glu	Ser	Leu	Trp	Pro	Leu	Ser	Val	Glu	Ser	Pro	
				805					810					815		
Ile	Gly	Arg	Cys	Gly	Glu	Pro	Asn	Arg	Cys	Ala	Pro	His	Phe	Glu	Trp	
			820					825					830			
Asn	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg	Asp	Gly	Glu	Lys	Cys	Ala	His	
		835					840					845				
His	Ser	His	His	Phe	Ser	Leu	Asp	Ile	Asp	Val	Gly	Cys	Thr	Asp	Leu	
	850					855					860					
His	Glu	Asn	Leu	Gly	Val	Trp	Val	Val	Phe	Lys	Ile	Lys	Thr	Gln	Glu	
865					870				875						880	
Gly	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu	Phe	Ile	Glu	Glu	Lys	Pro	Leu	
				885					890					895		
Leu	Gly	Glu	Ala	Leu	Ser	Arg	Val	Lys	Arg	Ala	Glu	Lys	Lys	Trp	Arg	
			900					905					910			
Asp	Lys	Arg	Glu	Lys	Leu	Gln	Leu	Glu	Thr	Lys	Arg	Val	Tyr	Thr	Glu	
		915					920						925			
Ala	Lys	Glu	Ala	Val	Asp	Ala	Leu	Phe	Val	Asp	Ser	Gln	Tyr	Asp	Arg	
	930					935					940					
Leu	Gln	Ala	Asp	Thr	Asn	Ile	Gly	Met	Ile	His	Ala	Ala	Asp	Lys	Leu	
945					950					955					960	
Val	His	Arg	Ile	Arg	Glu	Ala	Tyr	Leu	Ser	Glu	Leu	Pro	Val	Ile	Pro	
				965					970					975		
Gly	Val	Asn	Ala	Glu	Ile	Phe	Glu	Glu	Leu	Glu	Gly	His	Ile	Ile	Thr	
			980					985					990			
Ala	Ile	Ser	Leu	Tyr	Asp	Ala	Arg	Asn	Val	Val	Lys	Asn	Gly	Asp	Phe	
		995					1000					1005				
Asn	Asn	Gly	Leu	Thr	Cys	Trp	Asn	Val	Lys	Gly	His	Val	Asp	Val	Gln	
	1010					1015					1020					
Gln	Ser	His	His	Arg	Ser	Asp	Leu	Val	Ile	Pro	Glu	Trp	Glu	Ala	Glu	
1025					1030					1035					1040	
Val	Ser	Gln	Ala	Val	Arg	Val	Cys	Pro	Gly	Cys	Gly	Tyr	Ile	Leu	Arg	
				1045					1050					1055		
Val	Thr	Ala	Tyr	Lys	Glu	Gly	Tyr	Gly	Glu	Gly	Cys	Val	Thr	Ile	His	
			1060					1065					1070			
Glu	Ile	Glu	Asn	Asn	Thr	Asp	Glu	Leu	Lys	Phe	Lys	Asn	Arg	Glu	Glu	
		1075					1080					1085				
Glu	Glu	Val	Tyr	Pro	Thr	Asp	Thr	Gly	Thr	Cys	Asn	Asp	Tyr	Thr	Ala	
		1090					1095					1100				
His	Gln	Gly	Thr	Ala	Gly	Cys	Ala	Asp	Ala	Cys	Asn	Ser	Arg	Asn	Ala	
1105					1110					1115					1120	

Gly Tyr Glu Asp Ala Tyr Glu Val Asp Thr Thr Ala Ser Val Asn Tyr
1125 1130 1135

Lys Pro Thr Tyr Glu Glu Glu Thr Tyr Thr Asp Val Arg Arg Asp Asn
1140 1145 1150

His Cys Glu Tyr Asp Arg Gly Tyr Val Asn Tyr Pro Pro Val Pro Ala
1155 1160 1165

Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Thr Val
1170 1175 1180

Trp Ile Glu Ile Gly Glu Thr Glu Gly Lys Phe Ile Val Asp Ser Val
1185 1190 1195 1200

Glu Leu Leu Leu Met Glu Glu
1205

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3468 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..3465
(D) OTHER INFORMATION: /product= "Full-length, hybrid,
partially maize optimized cryIA(b)"
/note= "Disclosed in Figure 7 as contained in pCIB4434."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
1210 1215 1220	
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
1225 1230 1235	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
1240 1245 1250 1255	
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC	192
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
1260 1265 1270	
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC	240
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile	
1275 1280 1285	

GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1290 1295 1300	288
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 1305 1310 1315	336
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1320 1325 1330 1335	384
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 1340 1345 1350	432
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 1355 1360 1365	480
TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1370 1375 1380	528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1385 1390 1395	576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1400 1405 1410 1415	624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1420 1425 1430	672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1435 1440 1445	720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1450 1455 1460	768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 1465 1470 1475	816
CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 1480 1485 1490 1495	864
GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 1500 1505 1510	912
ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 1515 1520 1525	960

ATC ATG GCC AGC CCC GTC GGC TTC AGC GGC CCC GAG TTC ACC TTC CCC Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 1530 1535 1540	1008
CTG TAC GGC ACC ATG GGC AAC GCT GCA CCT CAG CAG CGC ATC GTG GCA Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 1545 1550 1555	1056
CAG CTG GGC CAG GGA GTG TAC CGC ACC CTG AGC AGC ACC CTG TAC CGT Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 1560 1565 1570 1575	1104
CGA CCT TTC AAC ATC GGC ATC AAC AAC CAG CAG CTG AGC GTG CTG GAC Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 1580 1585 1590	1152
GGC ACC GAG TTC GCC TAC GGC ACC AGC AGC AAC CTG CCC AGC GCC GTG Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 1595 1600 1605	1200
TAC CGC AAG AGC GGC ACC GTG GAC AGC CTG GAC GAG ATC CCC CCT CAG Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 1610 1615 1620	1248
AAC AAC AAC GTG CCA CCT CGA CAG GGC TTC AGC CAC CGT CTG AGC CAC Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 1625 1630 1635	1296
GTG AGC ATG TTC CGC AGT GGC TTC AGC AAC AGC AGC GTG AGC ATC ATC Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile 1640 1645 1650 1655	1344
CGT GCA CCT ATG TTC AGC TGG ATT CAC CGC AGT GCC GAG TTC AAC AAC Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 1660 1665 1670	1392
ATC ATC CCC AGC AGC CAG ATC ACC CAG ATC CCC CTG ACC AAG AGC ACC Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 1675 1680 1685	1440
AAC CTG GGC AGC GGC ACC AGC GTG GTG AAG GGC CCC GGC TTC ACC GGC Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 1690 1695 1700	1488
GGC GAC ATC CTG CGC CGC ACC AGC CCC GGC CAG ATC AGC ACC CTG CGC Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 1705 1710 1715	1536
GTG AAC ATC ACC GCC CCC CTG AGC CAG CGC TAC CGC GTC CGC ATC CGC Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 1720 1725 1730 1735	1584
TAC GCC AGC ACC ACC AAC CTG CAG TTC CAC ACC AGC ATC GAC GGC CGC Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg 1740 1745 1750	1632
CCC ATC AAC CAG GGC AAC TTC AGC GCC ACC ATG AGC AGC GGC AGC AAC Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn 1755 1760 1765	1680
CTG CAG AGC GGC AGC TTC CGC ACC GTG GGC TTC ACC ACC CCC TTC AAC	1728

Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn	
1770 1775 1780	
TTC AGC AAC GGC AGC AGC GTG TTC ACC CTG AGC GCC CAC GTG TTC AAC	1776
Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn	
1785 1790 1795	
AGC GGC AAC GAG GTG TAC ATC GAC CGC ATC GAG TTC GTG CCC GCC GAG	1824
Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu	
1800 1805 1810 1815	
GTG ACC TTC GAG GCC GAG TAC GAC CTG GAG AGG GCT CAG AAG GCC GTG	1872
Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val	
1820 1825 1830	
AAC GAG CTG TTC ACC AGC AGC AAC CAG ATC GGC CTG AAG ACC GAC GTG	1920
Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val	
1835 1840 1845	
ACC GAC TAC CAC ATC GAT CAA GTA TCC AAT TTA GTT GAG TGT TTA TCT	1968
Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser	
1850 1855 1860	
GAT GAA TTT TGT CTG GAT GAA AAA AAA GAA TTG TCC GAG AAA GTC AAA	2016
Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys	
1865 1870 1875	
CAT GCG AAG CGA CTT AGT GAT GAG CGG AAT TTA CTT CAA GAT CCA AAC	2064
His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn	
1880 1885 1890 1895	
TTT AGA GGG ATC AAT AGA CAA CTA GAC CGT GGC TGG AGA GGA AGT ACG	2112
Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr	
1900 1905 1910	
GAT ATT ACC ATC CAA GGA GGC GAT GAC GTA TTC AAA GAG AAT TAC GTT	2160
Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val	
1915 1920 1925	
ACG CTA TTG GGT ACC TTT GAT GAG TGC TAT CCA ACG TAT TTA TAT CAA	2208
Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln	
1930 1935 1940	
AAA ATA GAT GAG TCG AAA TTA AAA GCC TAT ACC CGT TAC CAA TTA AGA	2256
Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg	
1945 1950 1955	
GGG TAT ATC GAA GAT AGT CAA GAC TTA GAA ATC TAT TTA ATT CGC TAC	2304
Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr	
1960 1965 1970 1975	
AAT GCC AAA CAC GAA ACA GTA AAT GTG CCA GGT ACG GGT TCC TTA TGG	2352
Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp	
1980 1985 1990	
CCG CTT TCA GCC CCA AGT CCA ATC GGA AAA TGT GCC CAT CAT TCC CAT	2400
Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Ala His His Ser His	
1995 2000 2005	
CAT TTC TCC TTG GAC ATT GAT GTT GGA TGT ACA GAC TTA AAT GAG GAC	2448
His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp	

2010					2015					2020							
TTA Leu	GGT Gly	GTA Val	TGG Trp	GTG Val	ATA Ile	TTC Phe	AAG Lys	ATT Ile	AAG Lys	ACG Thr	CAA Gln	GAT Asp	GGC Gly	CAT His	GCA Ala	2496	
2025					2030					2035							
AGA Arg	CTA Leu	GGA Gly	AAT Asn	CTA Leu	GAA Glu	TTT Phe	CTC Leu	GAA Glu	GAG Glu	AAA Lys	CCA Pro	TTA Leu	GTA Val	GGA Gly	GAA Glu	2544	
2040					2045					2050					2055		
GCA Ala	CTA Leu	GCT Ala	CGT Arg	GTG Val	AAA Lys	AGA Arg	GCG Ala	GAG Glu	AAA Lys	AAA Lys	TGG Trp	AGA Arg	GAC Asp	AAA Lys	CGT Arg	2592	
2060					2065					2070							
GAA Glu	AAA Lys	TTG Leu	GAA Glu	TGG Trp	GAA Glu	ACA Thr	AAT Asn	ATT Ile	GTT Val	TAT Tyr	AAA Lys	GAG Glu	GCA Ala	AAA Lys	GAA Glu	2640	
2075					2080					2085							
TCT Ser	GTA Val	GAT Asp	GCT Ala	TTA Leu	TTT Phe	GTA Val	AAC Asn	TCT Ser	CAA Gln	TAT Tyr	GAT Asp	AGA Arg	TTA Leu	CAA Gln	GCG Ala	2688	
2090					2095					2100							
GAT Asp	ACC Thr	AAC Asn	ATC Ile	GCG Ala	ATG Met	ATT Ile	CAT His	GCG Ala	GCA Ala	GAT Asp	AAA Lys	CGC Arg	GTT Val	CAT His	AGC Ser	2736	
2105					2110					2115							
ATT Ile	CGA Arg	GAA Glu	GCT Ala	TAT Tyr	CTG Leu	CCT Pro	GAG Glu	CTG Leu	TCT Ser	GTG Val	ATT Ile	CCG Pro	GGT Gly	GTC Val	AAT Asn	2784	
2120					2125					2130					2135		
GCG Ala	GCT Ala	ATT Ile	TTT Phe	GAA Glu	GAA Glu	TTA Leu	GAA Glu	GGG Gly	CGT Arg	ATT Ile	TTC Phe	ACT Thr	GCA Ala	TTC Phe	TCC Ser	2832	
2140					2145					2150							
CTA Leu	TAT Tyr	GAT Asp	GCG Ala	AGA Arg	AAT Asn	GTC Val	ATT Ile	AAA Lys	AAT Asn	GGT Gly	GAT Asp	TTT Phe	AAT Asn	AAT Asn	GGC Gly	2880	
2155					2160					2165							
TTA Leu	TCC Ser	TGC Cys	TGG Trp	AAC Asn	GTG Val	AAA Lys	GGG Gly	CAT His	GTA Val	GAT Asp	GTA Val	GAA Glu	GAA Glu	CAA Gln	AAC Asn	2928	
2170					2175					2180							
AAC Asn	CAC His	CGT Arg	TCG Ser	GTC Val	CTT Leu	GTT Val	GTT Val	CCG Pro	GAA Glu	TGG Trp	GAA Glu	GCA Ala	GAA Glu	GTG Val	TCA Ser	2976	
2185					2190					2195							
CAA Gln	GAA Glu	GTT Val	CGT Arg	GTC Val	TGT Cys	CCG Pro	GGT Gly	CGT Arg	GGC Gly	TAT Tyr	ATC Ile	CTT Leu	CGT Arg	GTC Val	ACA Thr	3024	
2200					2205					2210					2215		
GCG Ala	TAC Tyr	AAG Lys	GAG Glu	GGA Gly	TAT Tyr	GGA Gly	GAA Glu	GGT Gly	TGC Cys	GTA Val	ACC Thr	ATT Ile	CAT His	GAG Glu	ATC Ile	3072	
2220					2225					2230							
GAG Glu	AAC Asn	AAT Asn	ACA Thr	GAC Asp	GAA Glu	CTG Leu	AAG Lys	TTT Phe	AGC Ser	AAC Asn	TGT Cys	GTA Val	GAA Glu	GAG Glu	GAA Glu	3120	
2235					2240					2245							
GTA Val	TAT Tyr	CCA Pro	AAC Asn	ACG Thr	GTA Val	ACG Thr	TGT Cys	AAT Asn	GAT Asp	TAT Tyr	ACT Thr	GCG Ala	ACT Thr	CAA Gln		3168	
2250					2255					2260							

GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly 2265 2270 2275	3216
GCC TAT GAA AGC AAT TCT TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT Ala Tyr Glu Ser Asn Ser Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr 2280 2285 2290 2295	3264
GAA GAA AAA GCA TAT ACA GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser 2300 2305 2310	3312
AAC AGA GGA TAT GGG GAT TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr 2315 2320 2325	3360
AAA GAA TTA GAG TAC TTC CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile 2330 2335 2340	3408
GGA GAA ACG GAA GGA ACA TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu 2345 2350 2355	3456
ATG GAG GAA TAA Met Glu Glu 2360	3468

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10 15
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 55 60
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 65 70 75 80
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 85 90 95
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 100 105 110

Ser	Phe	Arg	Glu	Trp	Glu	Ala	Asp	Pro	Thr	Asn	Pro	Ala	Leu	Arg	Glu		
		115					120					125					
Glu	Met	Arg	Ile	Gln	Phe	Asn	Asp	Met	Asn	Ser	Ala	Leu	Thr	Thr	Ala		
	130					135					140						
Ile	Pro	Leu	Phe	Ala	Val	Gln	Asn	Tyr	Gln	Val	Pro	Leu	Leu	Ser	Val		
145					150					155					160		
Tyr	Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Val	Leu	Arg	Asp	Val	Ser		
				165					170					175			
Val	Phe	Gly	Gln	Arg	Trp	Gly	Phe	Asp	Ala	Ala	Thr	Ile	Asn	Ser	Arg		
			180					185					190				
Tyr	Asn	Asp	Leu	Thr	Arg	Leu	Ile	Gly	Asn	Tyr	Thr	Asp	His	Ala	Val		
		195					200					205					
Arg	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	Val	Trp	Gly	Pro	Asp	Ser	Arg		
	210					215					220						
Asp	Trp	Ile	Arg	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Leu	Thr	Leu	Thr	Val		
225					230					235					240		
Leu	Asp	Ile	Val	Ser	Leu	Phe	Pro	Asn	Tyr	Asp	Ser	Arg	Thr	Tyr	Pro		
				245					250					255			
Ile	Arg	Thr	Val	Ser	Gln	Leu	Thr	Arg	Glu	Ile	Tyr	Thr	Asn	Pro	Val		
			260					265					270				
Leu	Glu	Asn	Phe	Asp	Gly	Ser	Phe	Arg	Gly	Ser	Ala	Gln	Gly	Ile	Glu		
		275					280					285					
Gly	Ser	Ile	Arg	Ser	Pro	His	Leu	Met	Asp	Ile	Leu	Asn	Ser	Ile	Thr		
	290					295					300						
Ile	Tyr	Thr	Asp	Ala	His	Arg	Gly	Glu	Tyr	Tyr	Trp	Ser	Gly	His	Gln		
305					310					315					320		
Ile	Met	Ala	Ser	Pro	Val	Gly	Phe	Ser	Gly	Pro	Glu	Phe	Thr	Phe	Pro		
				325					330					335			
Leu	Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala		
			340					345					350				
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg		
		355					360					365					
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp		
						375					380						
Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val		
385					390					395					400		
Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln		
				405					410				415				
Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His		
			420					425					430				

Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile
		435					440					445			
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn
	450					455					460				
Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr
465					470					475					480
Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly	Phe	Thr	Gly
				485					490					495	
Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg
			500					505					510		
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg
		515					520					525			
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg
	530					535					540				
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn
545					550					555					560
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn
				565					570					575	
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn
			580					585					590		
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu
		595					600					605			
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val
	610					615					620				
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val
625					630					635					640
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser
			645						650					655	
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys
			660					665					670		
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn
		675					680					685			
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr
	690					695					700				
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val
705					710					715					720
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln
				725					730					735	
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg
			740					745					750		
Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr

755					760					765					
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp
770						775					780				
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Ala	His	His	Ser	His
785					790					795					800
His	Phe	Ser	Leu	Asp	Ile	Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	Glu	Asp
				805					810					815	
Leu	Gly	Val	Trp	Val	Ile	Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly	His	Ala
			820					825					830		
Arg	Leu	Gly	Asn	Leu	Glu	Phe	Leu	Glu	Glu	Lys	Pro	Leu	Val	Gly	Glu
		835					840					845			
Ala	Leu	Ala	Arg	Val	Lys	Arg	Ala	Glu	Lys	Lys	Trp	Arg	Asp	Lys	Arg
		850				855					860				
Glu	Lys	Leu	Glu	Trp	Glu	Thr	Asn	Ile	Val	Tyr	Lys	Glu	Ala	Lys	Glu
865					870					875					880
Ser	Val	Asp	Ala	Leu	Phe	Val	Asn	Ser	Gln	Tyr	Asp	Arg	Leu	Gln	Ala
				885					890					895	
Asp	Thr	Asn	Ile	Ala	Met	Ile	His	Ala	Ala	Asp	Lys	Arg	Val	His	Ser
			900					905					910		
Ile	Arg	Glu	Ala	Tyr	Leu	Pro	Glu	Leu	Ser	Val	Ile	Pro	Gly	Val	Asn
		915					920					925			
Ala	Ala	Ile	Phe	Glu	Glu	Leu	Glu	Gly	Arg	Ile	Phe	Thr	Ala	Phe	Ser
		930				935					940				
Leu	Tyr	Asp	Ala	Arg	Asn	Val	Ile	Lys	Asn	Gly	Asp	Phe	Asn	Asn	Gly
945					950					955					960
Leu	Ser	Cys	Trp	Asn	Val	Lys	Gly	His	Val	Asp	Val	Glu	Glu	Gln	Asn
				965					970					975	
Asn	His	Arg	Ser	Val	Leu	Val	Val	Pro	Glu	Trp	Glu	Ala	Glu	Val	Ser
			980					985					990		
Gln	Glu	Val	Arg	Val	Cys	Pro	Gly	Arg	Gly	Tyr	Ile	Leu	Arg	Val	Thr
		995					1000					1005			
Ala	Tyr	Lys	Glu	Gly	Tyr	Gly	Glu	Gly	Cys	Val	Thr	Ile	His	Glu	Ile
		1010				1015					1020				
Glu	Asn	Asn	Thr	Asp	Glu	Leu	Lys	Phe	Ser	Asn	Cys	Val	Glu	Glu	Glu
1025					1030					1035					1040
Val	Tyr	Pro	Asn	Asn	Thr	Val	Thr	Cys	Asn	Asp	Tyr	Thr	Ala	Thr	Gln
				1045					1050					1055	
Glu	Glu	Tyr	Glu	Gly	Thr	Tyr	Thr	Ser	Arg	Asn	Arg	Gly	Tyr	Asp	Gly
			1060					1065					1070		
Ala	Tyr	Glu	Ser	Asn	Ser	Ser	Val	Pro	Ala	Asp	Tyr	Ala	Ser	Ala	Tyr
		1075					1080					1085			

Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser
 1090 1095 1100

Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr
 1105 1110 1115 1120

Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile
 1125 1130 1135

Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu
 1140 1145 1150

Met Glu Glu
 1155

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..3543
 - (D) OTHER INFORMATION: /product= "Full-length, hybrid, maize optimized heat stable cryIA(b)"
- /note= "Disclosed in Figure 9 as contained in pCIB5511."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
1160 1165 1170	
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
1175 1180 1185	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
1190 1195 1200	
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC	192
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
1205 1210 1215	
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC	240
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile	
1220 1225 1230 1235	
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC	288

Glu	Gln	Leu	Ile	Asn	Gln	Arg	Ile	Glu	Glu	Phe	Ala	Arg	Asn	Gln	Ala		
				1240					1245					1250			
ATC	AGC	CGC	CTG	GAG	GGC	CTG	AGC	AAC	CTG	TAC	CAA	ATC	TAC	GCC	GAG		336
Ile	Ser	Arg	Leu	Glu	Gly	Leu	Ser	Asn	Leu	Tyr	Gln	Ile	Tyr	Ala	Glu		
			1255					1260					1265				
AGC	TTC	CGC	GAG	TGG	GAG	GCC	GAC	CCC	ACC	AAC	CCC	GCC	CTG	CGC	GAG		384
Ser	Phe	Arg	Glu	Trp	Glu	Ala	Asp	Pro	Thr	Asn	Pro	Ala	Leu	Arg	Glu		
			1270				1275					1280					
GAG	ATG	CGC	ATC	CAG	TTC	AAC	GAC	ATG	AAC	AGC	GCC	CTG	ACC	ACC	GCC		432
Glu	Met	Arg	Ile	Gln	Phe	Asn	Asp	Met	Asn	Ser	Ala	Leu	Thr	Thr	Ala		
			1285			1290					1295						
ATC	CCC	CTG	TTC	GCC	GTG	CAG	AAC	TAC	CAG	GTG	CCC	CTG	CTG	AGC	GTG		480
Ile	Pro	Leu	Phe	Ala	Val	Gln	Asn	Tyr	Gln	Val	Pro	Leu	Leu	Ser	Val		
1300					1305					1310					1315		
TAC	GTG	CAG	GCC	GCC	AAC	CTG	CAC	CTG	AGC	GTG	CTG	CGC	GAC	GTC	AGC		528
Tyr	Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Val	Leu	Arg	Asp	Val	Ser		
				1320				1325						1330			
GTG	TTC	GGC	CAG	CGC	TGG	GGC	TTC	GAC	GCC	GCC	ACC	ATC	AAC	AGC	CGC		576
Val	Phe	Gly	Gln	Arg	Trp	Gly	Phe	Asp	Ala	Ala	Thr	Ile	Asn	Ser	Arg		
			1335				1340						1345				
TAC	AAC	GAC	CTG	ACC	CGC	CTG	ATC	GGC	AAC	TAC	ACC	GAC	CAC	GCC	GTG		624
Tyr	Asn	Asp	Leu	Thr	Arg	Leu	Ile	Gly	Asn	Tyr	Thr	Asp	His	Ala	Val		
			1350				1355					1360					
CGC	TGG	TAC	AAC	ACC	GGC	CTG	GAG	CGC	GTG	TGG	GGT	CCC	GAC	AGC	CGC		672
Arg	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	Val	Trp	Gly	Pro	Asp	Ser	Arg		
			1365			1370					1375						
GAC	TGG	ATC	AGG	TAC	AAC	CAG	TTC	CGC	CGC	GAG	CTG	ACC	CTG	ACC	GTG		720
Asp	Trp	Ile	Arg	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Leu	Thr	Leu	Thr	Val		
1380					1385					1390					1395		
CTG	GAC	ATC	GTG	AGC	CTG	TTC	CCC	AAC	TAC	GAC	AGC	CGC	ACC	TAC	CCC		768
Leu	Asp	Ile	Val	Ser	Leu	Phe	Pro	Asn	Tyr	Asp	Ser	Arg	Thr	Tyr	Pro		
				1400					1405					1410			
ATC	CGC	ACC	GTG	AGC	CAG	CTG	ACC	CGC	GAG	ATT	TAC	ACC	AAC	CCC	GTG		816
Ile	Arg	Thr	Val	Ser	Gln	Leu	Thr	Arg	Glu	Ile	Tyr	Thr	Asn	Pro	Val		
			1415				1420						1425				
CTG	GAG	AAC	TTC	GAC	GGC	AGC	TTC	CGC	GGC	AGC	GCC	CAG	GGC	ATC	GAG		864
Leu	Glu	Asn	Phe	Asp	Gly	Ser	Phe										

TTC	AGC	AAC	GGC	AGC	AGC	GTG	TTC	ACC	CTG	AGC	GCC	CAC	GTG	TTC	AAC	1776
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn	
			1735						1740						1745	
AGC	GGC	AAC	GAG	GTG	TAC	ATC	GAC	CGC	ATC	GAG	TTC	GTG	CCC	GCC	GAG	1824
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu	
			1750					1755					1760			
GTG	ACC	TTC	GAG	GCC	GAG	TAC	GAC	CTG	GAG	AGG	GCT	CAG	AAG	GCC	GTG	1872
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	
			1765					1770					1775			
AAC	GAG	CTG	TTC	ACC	AGC	AGC	AAC	CAG	ATC	GGC	CTG	AAG	ACC	GAC	GTG	1920
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	
						1785					1790				1795	
ACC	GAC	TAC	CAC	ATC	GAT	CAA	GTA	TCC	AAT	TTA	GTT	GAG	TGT	TTA	TCT	1968
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser	
						1800									1810	
GAT	GAA	TTT	TGT	CTG	GAT	GAA	AAA	AAA	GAA	TTG	TCC	GAG	AAA	GTC	AAA	2016
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys	
								1820						1825		
CAT	GCG	AAG	CGA	CTT	AGT	GAT	GAG	CGG	AAT	TTA	CTT	CAA	GAT	CCA	AAC	2064
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	
								1835						1840		
TTT	AGA	GGG	ATC	AAT	AGA	CAA	CTA	GAC	CGT	GGC	TGG	AGA	GGA	AGT	ACG	2112
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	
								1850						1855		
GAT	ATT	ACC	ATC	CAA	GGA	GGC	GAT	GAC	GTA	TTC	AAA	GAG	AAT	TAC	GTT	2160
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	
											1870				1875	
ACG	CTA	TTG	GGT	ACC	TTC	GAC	GAG	TGC	TAC	CCC	ACC	TAC	CTG	TAC	CAG	2208
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	
															1890	
AAG	ATC	GAC	GAG	AGC	AAG	CTG	AAG	GCC	TAC	ACC	CGC	TAC	CAG	CTG	CGC	2256
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg	
									1900						1905	
GGC	TAC	ATC	GAG	GAC	AGC	CAG	GAC	CTG	GAA	ATC	TAC	CTG	ATC	CGC	TAC	2304
Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	
								1915						1920		
AAC	GCC	AAG	CAC	GAG	ACC	GTG	AAC	GTG	CCC	GGC	ACC	GGC	AGC	CTG	TGG	2352
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp	
								1930						1935		
CCC	CTG	AGC	GCC	CCC	AGC	CCC	ATC	GGC	AAG	TGC	GGG	GAG	CCG	AAT	CGA	2400
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg	
											1950				1955	
TGC	GCT	CCG	CAC	CTG	GAG	TGG	AAC	CCG	GAC	CTA	GAC	TGC	AGC	TGC	AGG	2448
Cys	Ala	Pro	His	Leu	Glu	Trp	Asn	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg	
															1970	

GAC Asp	GGG Gly	GAG Glu	AAG Lys	TGC Cys	GCC Ala	CAC His	CAC His	AGC Ser	CAC His	TTC Phe	AGC Ser	CTG Leu	GAC Asp	ATC Ile	2496	
1975 1980 1985																
GAC Asp	GTG Val	GGC Gly	TGC Cys	ACC Thr	GAC Asp	CTG Leu	AAC Asn	GAG Glu	GAC Asp	CTG Leu	GGC Gly	GTG Val	TGG Trp	GTG Val	ATC Ile	2544
1990 1995 2000																
TTC Phe	AAG Lys	ATC Ile	AAG Lys	ACC Thr	CAG Gln	GAC Asp	GGC Gly	CAC His	GCC Ala	CGC Arg	CTG Leu	GGC Gly	AAT Asn	CTA Leu	GAA Glu	2592
2005 2010 2015																
TTT Phe	CTC Leu	GAA Glu	GAG Glu	AAA Lys	CCA Pro	TTA Leu	GTA Val	GGA Gly	GAA Glu	GCA Ala	CTA Leu	GCT Ala	CGT Arg	GTG Val	AAA Lys	2640
2020 2025 2030 2035																
AGA Arg	GCG Ala	GAG Glu	AAA Lys	AAA Lys	TGG Trp	AGA Arg	GAC Asp	AAA Lys	CGT Arg	GAA Glu	AAA Lys	TTG Leu	GAA Glu	TGG Trp	GAA Glu	2688
2040 2045 2050																
ACA Thr	AAT Asn	ATT Ile	GTT Val	TAT Tyr	AAA Lys	GAG Glu	GCA Ala	AAA Lys	GAA Glu	TCT Ser	GTA Val	GAT Asp	GCT Ala	TTA Leu	TTT Phe	2736
2055 2060 2065																
GTA Val	AAC Asn	TCT Ser	CAA Gln	TAT Tyr	GAT Asp	AGA Arg	TTA Leu	CAA Gln	GCG Ala	GAT Asp	ACC Thr	AAC Asn	ATC Ile	GCG Ala	ATG Met	2784
2070 2075 2080																
ATT Ile	CAT His	GCG Ala	GCA Ala	GAT Asp	AAA Lys	CGC Arg	GTT Val	CAT His	AGC Ser	ATT Ile	CGA Arg	GAA Glu	GCT Ala	TAT Tyr	CTG Leu	2832
2085 2090 2095																
CCT Pro	GAG Glu	CTG Leu	TCT Ser	GTG Val	ATT Ile	CCG Pro	GGT Gly	GTC Val	AAT Asn	GCG Ala	GCT Ala	ATT Ile	TTT Phe	GAA Glu	GAA Glu	2880
2100 2105 2110 2115																
TTA Leu	GAA Glu	GGG Gly	CGT Arg	ATT Ile	TTC Phe	ACT Thr	GCA Ala	TTC Phe	TCC Ser	CTA Leu	TAT Tyr	GAT Asp	GCG Ala	AGA Arg	AAT Asn	2928
2120 2125 2130																
GTC Val	ATT Ile	AAA Lys	AAT Asn	GGT Gly	GAT Asp	TTT Phe	AAT Asn	AAT Asn	GGC Gly	TTA Leu	TCC Ser	TGC Cys	TGG Trp	AAC Asn	GTG Val	2976
2135 2140 2145																
AAA Lys	GGG Gly	CAT His	GTA Val	GAT Asp	GTA Val	GAA Glu	GAA Glu	CAA Gln	AAC Asn	AAC Asn	CAC His	CGT Arg	TCG Ser	GTC Val	CTT Leu	3024
2150 2155 2160																
GTT Val	GTT Val	CCG Pro	GAA Glu	TGG Trp	GAA Glu	GCA Ala	GAA Glu	GTG Val	TCA Ser	CAA Gln	GAA Glu	GTT Val	CGT Arg	GTC Val	TGT Cys	3072
2165 2170 2175																
CCG Pro	GGT Gly	CGT Arg	GGC Gly	TAT Tyr	ATC Ile	CTT Leu	CGT Arg	GTC Val	ACA Thr	GCG Ala	TAC Tyr	AAG Lys	GAG Glu	GGA Gly	TAT Tyr	3120
2180 2185 2190 2195																
GGA Gly	GAA Glu	GGT Gly	TGC Cys	GTA Val	ACC Thr	ATT Ile	CAT His	GAG Glu	ATC Ile	GAG Glu	AAC Asn	AAT Asn	ACA Thr	GAC Asp	GAA Glu	3168
2200 2205 2210																
CTG	AAG	TTT	AGC	AAC	TGT	GTA	GAA	GAG	GAA	GTA	TAT	CCA	AAC	AAC	ACG	3216

Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr	
2215 2220 2225	
GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA GAA GAA TAT GAG GGT ACG	3264
Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr	
2230 2235 2240	
TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA GCC TAT GAA AGC AAT TCT	3312
Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser	
2245 2250 2255	
TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT GAA GAA AAA GCA TAT ACA	3360
Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr	
2260 2265 2270 2275	
GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT AAC AGA GGA TAT GGG GAT	3408
Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp	
2280 2285 2290	
TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA AAA GAA TTA GAG TAC TTC	3456
Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe	
2295 2300 2305	
CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC GGA GAA ACG GAA GGA ACA	3504
Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr	
2310 2315 2320	
TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT ATG GAG GAA TAA	3546
Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu	
2325 2330 2335	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
1 5 10 15	
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
20 25 30	
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
35 40 45	
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
50 55 60	
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile	
65 70 75 80	
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala	
85 90 95	

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
115 120 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
165 170 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His

420					425					430					
Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile
		435					440					445			
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn
	450					455					460				
Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr
465						470					475				480
Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly	Phe	Thr	Gly
				485					490					495	
Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg
			500					505					510		
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg
		515					520					525			
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg
	530					535					540				
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn
545						550					555				560
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn
				565					570					575	
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn
			580					585					590		
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu
		595					600					605			
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val
	610					615					620				
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val
625						630					635				640
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser
				645					650					655	
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys
			660					665					670		
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn
		675					680					685			
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr
	690					695					700				
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val
705						710					715				720
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln
				725					730					735	
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg
			740					745					750		

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
755 760 765

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
770 775 780

Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg
785 790 795 800

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg
805 810 815

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
820 825 830

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
835 840 845

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
850 855 860

Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys
865 870 875 880

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu
885 890 895

Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
900 905 910

Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met
915 920 925

Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu
930 935 940

Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu
945 950 955 960

Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
965 970 975

Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val
980 985 990

Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu
995 1000 1005

Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys
1010 1015 1020

Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr
1025 1030 1035 1040

Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu
1045 1050 1055

Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr
1060 1065 1070

Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr
1075 1080 1085

Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser
1090 1095 1100

Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr
1105 1110 1115 1120

Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp
1125 1130 1135

Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe
1140 1145 1150

Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr
1155 1160 1165

Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1170 1175 1180

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3543
- (D) OTHER INFORMATION: /product= "Full-length, hybrid,
maize optimized heat stable cryIA(b)"
/note= "Disclosed in Figure 11 as contained in pCIB5512"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
1185 1190 1195	
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
1200 1205 1210	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
1215 1220 1225	
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC	192
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
1230 1235 1240 1245	

TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 1250 1255 1260	240
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1265 1270 1275	288
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 1280 1285 1290	336
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1295 1300 1305	384
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 1310 1315 1320 1325	432
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 1330 1335 1340	480
TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1345 1350 1355	528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1360 1365 1370	576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1375 1380 1385	624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1390 1395 1400 1405	672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1410 1415 1420	720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1425 1430 1435	768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 1440 1445 1450	816
CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 1455 1460 1465	864
GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 1470 1475 1480 1485	912
ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG	960

Ile	Tyr	Thr	Asp	Ala	His	Arg	Gly	Glu	Tyr	Tyr	Trp	Ser	Gly	His	Gln	
				1490					1495					1500		
ATC	ATG	GCC	AGC	CCC	GTC	GGC	TTC	AGC	GGC	CCC	GAG	TTC	ACC	TTC	CCC	1008
Ile	Met	Ala	Ser	Pro	Val	Gly	Phe	Ser	Gly	Pro	Glu	Phe	Thr	Phe	Pro	
			1505					1510					1515			
CTG	TAC	GGC	ACC	ATG	GGC	AAC	GCT	GCA	CCT	CAG	CAG	CGC	ATC	GTG	GCA	1056
Leu	Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala	
		1520					1525					1530				
CAG	CTG	GGC	CAG	GGA	GTG	TAC	CGC	ACC	CTG	AGC	AGC	ACC	CTG	TAC	CGT	1104
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg	
	1535					1540					1545					
CGA	CCT	TTC	AAC	ATC	GGC	ATC	AAC	AAC	CAG	CAG	CTG	AGC	GTG	CTG	GAC	1152
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp	
1550				1555					1560						1565	
GGC	ACC	GAG	TTC	GCC	TAC	GGC	ACC	AGC	AGC	AAC	CTG	CCC	AGC	GCC	GTG	1200
Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val	
				1570				1575						1580		
TAC	CGC	AAG	AGC	GGC	ACC	GTG	GAC	AGC	CTG	GAC	GAG	ATC	CCC	CCT	CAG	1248
Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln	
			1585				1590					1595				
AAC	AAC	AAC	GTG	CCA	CCT	CGA	CAG	GGC	TTC	AGC	CAC	CGT	CTG	AGC	CAC	1296
Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His	
		1600					1605					1610				
GTG	AGC	ATG	TTC	CGC	AGT	GGC	TTC	AGC	AAC	AGC	AGC	GTG	AGC	ATC	ATC	1344
Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile	
	1615					1620					1625					
CGT	GCA	CCT	ATG	TTC	AGC	TGG	ATT	CAC	CGC	AGT	GCC	GAG	TTC	AAC	AAC	1392
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn	
1630				1635				1640						1645		
ATC	ATC	CCC	AGC	AGC	CAG	ATC	ACC	CAG	ATC	CCC	CTG	ACC	AAG	AGC	ACC	1440
Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr	
				1650				1655						1660		
AAC	CTG	GGC	AGC	GGC	ACC	AGC	GTG	GTG	AAG	GGC	CCC	GGC	TTC	ACC	GGC	1488
Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly	Phe	Thr	Gly	
		1665					1670					1675				
GGC	GAC	ATC	CTG	CGC	CGC	ACC	AGC	CCC	GGC	CAG	ATC	AGC	ACC	CTG	CGC	1536
Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg	
		1680					1685					1690				
GTG	AAC	ATC	ACC	GCC	CCC	CTG	AGC	CAG	CGC	TAC	CGC	GTC	CGC	ATC	CGC	1584
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	
	1695					1700					1705					
TAC	GCC	AGC	ACC	ACC	AAC	CTG	CAG	TTC	CAC	ACC	AGC	ATC	GAC	GGC	CGC	1632
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg	
1710					1715			1720						1725		
CCC	ATC	AAC	CAG	GGC	AAC	TTC	AGC	GCC	ACC	ATG	AGC	AGC	GGC	AGC	AAC	1680
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn	

1730						1735						1740						
CTG	CAG	AGC	GGC	AGC	TTC	CGC	ACC	GTG	GGC	TTC	ACC	ACC	CCC	TTC	AAC	1728		
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn			
1745						1750						1755						
TTC	AGC	AAC	GGC	AGC	AGC	GTG	TTC	ACC	CTG	AGC	GCC	CAC	GTG	TTC	AAC	1776		
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn			
1760						1765						1770						
AGC	GGC	AAC	GAG	GTG	TAC	ATC	GAC	CGC	ATC	GAG	TTC	GTG	CCC	GCC	GAG	1824		
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu			
1775						1780						1785						
GTG	ACC	TTC	GAG	GCC	GAG	TAC	GAC	CTG	GAG	AGG	GCT	CAG	AAG	GCC	GTG	1872		
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val			
1790						1795						1800						1805
AAC	GAG	CTG	TTC	ACC	AGC	AGC	AAC	CAG	ATC	GGC	CTG	AAG	ACC	GAC	GTG	1920		
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val			
1810						1815						1820						
ACC	GAC	TAC	CAC	ATC	GAT	CAG	GTG	AGC	AAC	CTG	GTG	GAG	TGC	TTA	AGC	1968		
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser			
1825						1830						1835						
GAC	GAG	TTC	TGC	CTG	GAC	GAG	AAG	AAG	GAG	CTG	AGC	GAG	AAG	GTG	AAG	2016		
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys			
1840						1845						1850						
CAC	GCC	AAG	CGC	CTG	AGC	GAC	GAG	CGC	AAC	CTG	CTG	CAG	GAC	CCC	AAC	2064		
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn			
1855						1860						1865						
TTC	CGC	GGC	ATC	AAC	CGC	CAG	CTG	GAC	CGC	GGC	TGG	CGA	GGC	AGC	ACC	2112		
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr			
1870						1875						1880						1885
GAT	ATC	ACC	ATC	CAG	GGC	GGC	GAC	GAC	GTG	TTC	AAG	GAG	AAC	TAC	GTG	2160		
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val			
1890						1895						1900						
ACC	CTG	CTG	GGC	ACC	TTC	GAC	GAG	TGC	TAC	CCC	ACC	TAC	CTG	TAC	CAG	2208		
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln			
1905						1910						1915						
AAG	ATC	GAC	GAG	AGC	AAG	CTG	AAG	GCC	TAC	ACC	CGC	TAC	CAG	CTG	CGC	2256		
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg			
1920						1925						1930						
GGC	TAC	ATC	GAG	GAC	AGC	CAG	GAC	CTG	GAA	ATC	TAC	CTG	ATC	CGC	TAC	2304		
Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr			
1935						1940						1945						
AAC	GCC	AAG	CAC	GAG	ACC	GTG	AAC	GTG	CCC	GGC	ACC	GGC	AGC	CTG	TGG	2352		
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp			
1950						1955						1960						1965
CCC	CTG	AGC	GCC	CCC	AGC	CCC	ATC	GGC	AAG	TGC	GGG	GAG	CCG	AAT	CGA	2400		
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg			
1970						1975						1980						

TGC GCT CCG CAC CTG GAG TGG AAC CCG GAC CTA GAC TGC AGC TGC AGG Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg 1985 1990 1995	2448
GAC GGG GAG AAG TGC GCC CAC CAC AGC CAC CAC TTC AGC CTG GAC ATC Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile 2000 2005 2010	2496
GAC GTG GGC TGC ACC GAC CTG AAC GAG GAC CTG GGC GTG TGG GTG ATC Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile 2015 2020 2025	2544
TTC AAG ATC AAG ACC CAG GAC GGC CAC GCC CGC CTG GGC AAT CTA GAA Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu 2030 2035 2040 2045	2592
TTT CTC GAA GAG AAA CCA TTA GTA GGA GAA GCA CTA GCT CGT GTG AAA Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys 2050 2055 2060	2640
AGA GCG GAG AAA AAA TGG AGA GAC AAA CGT GAA AAA TTG GAA TGG GAA Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 2065 2070 2075	2688
ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA TCT GTA GAT GCT TTA TTT Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe 2080 2085 2090	2736
GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG GAT ACC AAC ATC GCG ATG Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 2095 2100 2105	2784
ATT CAT GCG GCA GAT AAA CGC GTT CAT AGC ATT CGA GAA GCT TAT CTG Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 2110 2115 2120 2125	2832
CCT GAG CTG TCT GTG ATT CCG GGT GTC AAT GCG GCT ATT TTT GAA GAA Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 2130 2135 2140	2880
TTA GAA GGG CGT ATT TTC ACT GCA TTC TCC CTA TAT GAT GCG AGA AAT Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn 2145 2150 2155	2928
GTC ATT AAA AAT GGT GAT TTT AAT AAT GGC TTA TCC TGC TGG AAC GTG Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 2160 2165 2170	2976
AAA GGG CAT GTA GAT GTA GAA GAA CAA AAC AAC CAC CGT TCG GTC CTT Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 2175 2180 2185	3024
GTT GTT CCG GAA TGG GAA GCA GAA GTG TCA CAA GAA GTT CGT GTC TGT Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 2190 2195 2200 2205	3072
CCG GGT CGT GGC TAT ATC CTT CGT GTC ACA GCG TAC AAG GAG GGA TAT Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 2210 2215 2220	3120

GGA GAA GGT TGC GTA ACC ATT CAT GAG ATC GAG AAC AAT ACA GAC GAA Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 2225 2230 2235	3168
CTG AAG TTT AGC AAC TGT GTA GAA GAG GAA GTA TAT CCA AAC AAC ACG Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr 2240 2245 2250	3216
GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA GAA GAA TAT GAG GGT ACG Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr 2255 2260 2265	3264
TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA GCC TAT GAA AGC AAT TCT Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 2270 2275 2280 2285	3312
TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT GAA GAA AAA GCA TAT ACA Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 2290 2295 2300	3360
GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT AAC AGA GGA TAT GGG GAT Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp 2305 2310 2315	3408
TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA AAA GAA TTA GAG TAC TTC Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe 2320 2325 2330	3456
CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC GGA GAA ACG GAA GGA ACA Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr 2335 2340 2345	3504
TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT ATG GAG GAA TAA Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu 2350 2355 2360	3546

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10 15
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 55 60
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile

65						70						75						80
Glu	Gln	Leu	Ile	Asn	Gln	Arg	Ile	Glu	Glu	Phe	Ala	Arg	Asn	Gln	Ala			
				85					90					95				
Ile	Ser	Arg	Leu	Glu	Gly	Leu	Ser	Asn	Leu	Tyr	Gln	Ile	Tyr	Ala	Glu			
				100					105					110				
Ser	Phe	Arg	Glu	Trp	Glu	Ala	Asp	Pro	Thr	Asn	Pro	Ala	Leu	Arg	Glu			
				115					120					125				
Glu	Met	Arg	Ile	Gln	Phe	Asn	Asp	Met	Asn	Ser	Ala	Leu	Thr	Thr	Ala			
				130					135					140				
Ile	Pro	Leu	Phe	Ala	Val	Gln	Asn	Tyr	Gln	Val	Pro	Leu	Leu	Ser	Val			
145					150					155					160			
Tyr	Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Val	Leu	Arg	Asp	Val	Ser			
				165					170					175				
Val	Phe	Gly	Gln	Arg	Trp	Gly	Phe	Asp	Ala	Ala	Thr	Ile	Asn	Ser	Arg			
				180					185					190				
Tyr	Asn	Asp	Leu	Thr	Arg	Leu	Ile	Gly	Asn	Tyr	Thr	Asp	His	Ala	Val			
				195					200					205				
Arg	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	Val	Trp	Gly	Pro	Asp	Ser	Arg			
				210					215					220				
Asp	Trp	Ile	Arg	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Leu	Thr	Leu	Thr	Val			
225					230					235					240			
Leu	Asp	Ile	Val	Ser	Leu	Phe	Pro	Asn	Tyr	Asp	Ser	Arg	Thr	Tyr	Pro			
				245					250					255				
Ile	Arg	Thr	Val	Ser	Gln	Leu	Thr	Arg	Glu	Ile	Tyr	Thr	Asn	Pro	Val			
				260					265					270				
Leu	Glu	Asn	Phe	Asp	Gly	Ser	Phe	Arg	Gly	Ser	Ala	Gln	Gly	Ile	Glu			
				275					280					285				
Gly	Ser	Ile	Arg	Ser	Pro	His	Leu	Met	Asp	Ile	Leu	Asn	Ser	Ile	Thr			
				290					295					300				
Ile	Tyr	Thr	Asp	Ala	His	Arg	Gly	Glu	Tyr	Tyr	Trp	Ser	Gly	His	Gln			
305					310					315					320			
Ile	Met	Ala	Ser	Pro	Val	Gly	Phe	Ser	Gly	Pro	Glu	Phe	Thr	Phe	Pro			
				325					330					335				
Leu	Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala			
				340					345					350				
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg			
				355					360					365				
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp			
				370					375					380				
Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val			
385					390					395					400			

Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln	
				405					410						415	
Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His	
			420					425					430			
Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile	
		435					440					445				
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn	
	450					455					460					
Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr	
465					470					475					480	
Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly	Phe	Thr	Gly	
				485					490					495		
Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg	
			500					505					510			
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	
		515					520					525				
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg	
	530					535					540					
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn	
545					550					555					560	
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn	
				565					570					575		
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn	
			580					585					590			
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu	
		595					600					605				
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	
	610					615					620					
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	
625					630					635					640	
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser	
				645					650					655		
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys	
			660					665					670			
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	
		675					680					685				
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	
	690					695					700					
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	
705					710					715					720	

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
 725 730 735
 Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
 740 745 750
 Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
 755 760 765
 Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
 770 775 780
 Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg
 785 790 795 800
 Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg
 805 810 815
 Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
 820 825 830
 Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
 835 840 845
 Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
 850 855 860
 Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys
 865 870 875 880
 Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu
 885 890 895
 Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
 900 905 910
 Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met
 915 920 925
 Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu
 930 935 940
 Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu
 945 950 955 960
 Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
 965 970 975
 Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val
 980 985 990
 Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu
 995 1000 1005
 Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys
 1010 1015 1020
 Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr
 1025 1030 1035 1040
 Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu

1045	1050	1055
Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr		
1060	1065	1070
Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr		
1075	1080	1085
Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser		
1090	1095	1100
Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr		
1105	1110	1115
Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp		
1125	1130	1135
Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe		
1140	1145	1150
Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr		
1155	1160	1165
Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu		
1170	1175	1180

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3546 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..3543
 - (D) OTHER INFORMATION: /product= "Full-length, hybrid, maize optimized heat stable cryIA(b)"
 - /note= "Disclosed in Figure 13 as contained in pCIB5513."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
1185	1190
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
1200	1205
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
1215	1220

GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 1230 1235 1240 1245	192
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 1250 1255 1260	240
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1265 1270 1275	288
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 1280 1285 1290	336
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1295 1300 1305	384
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 1310 1315 1320 1325	432
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 1330 1335 1340	480
TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1345 1350 1355	528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1360 1365 1370	576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1375 1380 1385	624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1390 1395 1400 1405	672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1410 1415 1420	720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1425 1430 1435	768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 1440 1445 1450	816
CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 1455 1460 1465	864

GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 1470 1475 1480 1485	912
ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 1490 1495 1500	960
ATC ATG GCC AGC CCC GTC GGC TTC AGC GGC CCC GAG TTC ACC TTC CCC Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 1505 1510 1515	1008
CTG TAC GGC ACC ATG GGC AAC GCT GCA CCT CAG CAG CGC ATC GTG GCA Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 1520 1525 1530	1056
CAG CTG GGC CAG GGA GTG TAC CGC ACC CTG AGC AGC ACC CTG TAC CGT Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 1535 1540 1545	1104
CGA CCT TTC AAC ATC GGC ATC AAC AAC CAG CAG CTG AGC GTG CTG GAC Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 1550 1555 1560 1565	1152
GGC ACC GAG TTC GCC TAC GGC ACC AGC AGC AAC CTG CCC AGC GCC GTG Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 1570 1575 1580	1200
TAC CGC AAG AGC GGC ACC GTG GAC AGC CTG GAC GAG ATC CCC CCT CAG Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 1585 1590 1595	1248
AAC AAC AAC GTG CCA CCT CGA CAG GGC TTC AGC CAC CGT CTG AGC CAC Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 1600 1605 1610	1296
GTG AGC ATG TTC CGC AGT GGC TTC AGC AAC AGC AGC GTG AGC ATC ATC Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile 1615 1620 1625	1344
CGT GCA CCT ATG TTC AGC TGG ATT CAC CGC AGT GCC GAG TTC AAC AAC Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 1630 1635 1640 1645	1392
ATC ATC CCC AGC AGC CAG ATC ACC CAG ATC CCC CTG ACC AAG AGC ACC Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 1650 1655 1660	1440
AAC CTG GGC AGC GGC ACC AGC GTG GTG AAG GGC CCC GGC TTC ACC GGC Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 1665 1670 1675	1488
GGC GAC ATC CTG CGC CGC ACC AGC CCC GGC CAG ATC AGC ACC CTG CGC Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 1680 1685 1690	1536
GTG AAC ATC ACC GCC CCC CTG AGC CAG CGC TAC CGC GTC CGC ATC CGC Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 1695 1700 1705	1584
TAC GCC AGC ACC ACC AAC CTG CAG TTC CAC ACC AGC ATC GAC GGC CGC	1632

Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg	
1710	1715 1720 1725
CCC ATC AAC CAG GGC AAC TTC AGC GCC ACC ATG AGC AGC GGC AGC AAC	1680
Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn	
1730	1735 1740
CTG CAG AGC GGC AGC TTC CGC ACC GTG GGC TTC ACC ACC CCC TTC AAC	1728
Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn	
1745	1750 1755
TTC AGC AAC GGC AGC AGC GTG TTC ACC CTG AGC GCC CAC GTG TTC AAC	1776
Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn	
1760	1765 1770
AGC GGC AAC GAG GTG TAC ATC GAC CGC ATC GAG TTC GTG CCC GCC GAG	1824
Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu	
1775	1780 1785
GTG ACC TTC GAG GCC GAG TAC GAC CTG GAG AGG GCT CAG AAG GCC GTG	1872
Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val	
1790	1795 1800 1805
AAC GAG CTG TTC ACC AGC AGC AAC CAG ATC GGC CTG AAG ACC GAC GTG	1920
Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val	
1810	1815 1820
ACC GAC TAC CAC ATC GAC CAG GTG AGC AAC CTG GTG GAG TGC TTA AGC	1968
Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser	
1825	1830 1835
GAC GAG TTC TGC CTG GAC GAG AAG AAG GAG CTG AGC GAG AAG GTG AAG	2016
Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys	
1840	1845 1850
CAC GCC AAG CGC CTG AGC GAC GAG CGC AAC CTG CTG CAG GAC CCC AAC	2064
His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn	
1855	1860 1865
TTC CGC GGC ATC AAC CGC CAG CTG GAC CGC GGC TGG CGA GGC AGC ACC	2112
Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr	
1870	1875 1880 1885
GAT ATC ACC ATC CAG GGC GGC GAC GAC GTG TTC AAG GAG AAC TAC GTG	2160
Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val	
1890	1895 1900
ACC CTG CAG GGC ACC TTC GAC GAG TGC TAC CCC ACC TAC CTG TAC CAG	2208
Thr Leu Gln Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln	
1905	1910 1915
CCG ATC GAC GAG AGC AAG CTG AAG GCC TAC ACC CGC TAC CAG CTG CGC	2256
Pro Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg	
1920	1925 1930
GGC TAC ATC GAG GAC AGC CAG GAC CTG GAA ATC TAC CTG ATC CGC TAC	2304
Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr	
1935	1940 1945
AAC GCC AAG CAC GAG ACC GTG AAC GTG CCC GGC ACC GGC AGC CTG TGG	2352
Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp	

1950				1955				1960				1965					
CCC Pro	CTG Leu	AGC Ser	GCC Ala	CCC Pro	AGC Ser	CCC Pro	ATC Ile	GGC Gly	AAG Lys	TGC Cys	GGG Gly	GAG Glu	CCG Pro	AAT Asn	CGA Arg	2400	
				1970				1975				1980					
TGC Cys	GCT Ala	CCG Pro	CAC His	CTG Leu	GAG Glu	TGG Trp	AAC Asn	CCG Pro	GAC Asp	CTA Leu	GAC Asp	TGC Cys	AGC Ser	TGC Cys	AGG Arg	2448	
				1985				1990				1995					
GAC Asp	GGG Gly	GAG Glu	AAG Lys	TGC Cys	GCC Ala	CAC His	CAC His	AGC Ser	CAC His	CAC His	TTC Phe	AGC Ser	CTG Leu	GAC Asp	ATC Ile	2496	
				2000				2005				2010					
GAC Asp	GTG Val	GGC Gly	TGC Cys	ACC Thr	GAC Asp	CTG Leu	AAC Asn	GAG Glu	GAC Asp	CTG Leu	GGC Gly	GTG Val	TGG Trp	GTG Val	ATC Ile	2544	
				2015				2020				2025					
TTC Phe	AAG Lys	ATC Ile	AAG Lys	ACC Thr	CAG Gln	GAC Asp	GGC Gly	CAC His	GCC Ala	CGC Arg	CTG Leu	GGC Gly	AAT Asn	CTA Leu	GAG Glu	2592	
				2030				2035				2040				2045	
TTC Phe	CTG Leu	GAG Glu	GAG Glu	AAG Lys	CCC Pro	CTG Leu	GTG Val	GGC Gly	GAG Glu	GCC Ala	CTG Leu	GCC Ala	CGC Arg	GTG Val	AAG Lys	2640	
				2050				2055				2060					
CGC Arg	GCC Ala	GAG Glu	AAG Lys	AAG Lys	TGG Trp	CGC Arg	GAC Asp	AAG Lys	CGC Arg	GAG Glu	AAG Lys	CTG Leu	GAG Glu	TGG Trp	GAG Glu	2688	
				2065				2070				2075					
ACC Thr	AAC Asn	ATC Ile	GTG Val	TAC Tyr	AAG Lys	GAG Glu	GCC Ala	AAG Lys	GAG Glu	AGC Ser	GTG Val	GAC Asp	GCC Ala	CTG Leu	TTC Phe	2736	
				2080				2085				2090					
GTG Val	AAC Asn	AGC Ser	CAG Gln	TAC Tyr	GAC Asp	CGC Arg	CTG Leu	CAG Gln	GCC Ala	GAC Asp	ACC Thr	AAC Asn	ATC Ile	GCC Ala	ATG Met	2784	
				2095				2100				2105					
ATC Ile	CAC His	GCC Ala	GCC Ala	GAC Asp	AAG Lys	CGC Arg	GTG Val	CAC His	AGC Ser	ATT Ile	CGC Arg	GAG Glu	GCC Ala	TAC Tyr	CTG Leu	2832	
				2110				2115				2120				2125	
CCC Pro	GAG Glu	CTG Leu	AGC Ser	GTG Val	ATC Ile	CCC Pro	GGC Gly	GTG Val	AAC Asn	GCC Ala	GCC Ala	ATC Ile	TTC Phe	GAG Glu	GAA Glu	2880	
				2130				2135				2140					
CTC Leu	GAG Glu	GGC Gly	CGC Arg	ATC Ile	TTC Phe	ACC Thr	GCC Ala	TTC Phe	AGC Ser	CTG Leu	TAC Tyr	GAC Asp	GCC Ala	CGC Arg	AAC Asn	2928	
				2145				2150				2155					
GTG Val	ATC Ile	AAG Lys	AAC Asn	GGC Gly	GAC Asp	TTC Phe	AAC Asn	AAC Asn	GGC Gly	CTG Leu	AGC Ser	TGC Cys	TGG Trp	AAC Asn	GTG Val	2976	
				2160				2165				2170					
AAG Lys	GGC Gly	CAC His	GTG Val	GAC Asp	GTG Val	GAG Glu	GAG Glu	CAG Gln	AAC Asn	AAC Asn	CAC His	CGC Arg	AGC Ser	GTG Val	CTG Leu	3024	
				2175				2180				2185					
GTG Val	GTG Val	CCC Pro	GAG Glu	TGG Trp	GAG Glu	GCC Ala	GAG Glu	GTG Val	AGC Ser	CAG Gln	GAG Glu	GTG Val	CGC Arg	GTG Val	TGC Cys	3072	
				2190				2195				2200				2205	

CCC GGC CGC GGC TAC ATC CTG CGC GTG ACC GCC TAC AAG GAG GGC TAC Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 2210 2215 2220	3120
GGC GAG GGC TGC GTG ACC ATC CAC GAG ATC GAG AAC AAC ACC GAC GAG Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 2225 2230 2235	3168
CTC AAG TTC AGC AAC TGC GTG GAG GAG GAG GTT TAC CCC AAC AAC ACC Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr 2240 2245 2250	3216
GTG ACC TGC AAC GAC TAC ACC GCG ACC CAG GAG GAG TAC GAA GGC ACC Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr 2255 2260 2265	3264
TAC ACC TCT CGC AAC AGG GGT TAC GAC GGC GCC TAC GAG TCC AAC AGC Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 2270 2275 2280 2285	3312
TCC GTG CCA GCC GAC TAC GCC AGC GCC TAC GAG GAG AAA GCC TAC ACC Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 2290 2295 2300	3360
GAC GGT AGA CGC GAC AAC CCA TGT GAG AGC AAC AGA GGC TAC GGC GAC Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp 2305 2310 2315	3408
TAC ACC CCC CTG CCC GCT GGA TAC GTG ACC AAG GAG CTG GAG TAC TTC Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe 2320 2325 2330	3456
CCC GAG ACC GAC AAG GTG TGG ATC GAG ATT GGC GAG ACC GAG GGC ACC Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr 2335 2340 2345	3504
TTC ATC GTG GAC AGC GTG GAG CTG CTG CTG ATG GAG GAG TAG Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu 2350 2355 2360	3546

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10 15
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
 50 55 60
 Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
 65 70 75 80
 Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
 85 90 95
 Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
 100 105 110
 Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
 115 120 125
 Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
 130 135 140
 Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
 145 150 155 160
 Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
 165 170 175
 Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
 180 185 190
 Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val
 195 200 205
 Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
 210 215 220
 Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
 225 230 235 240
 Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro
 245 250 255
 Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
 260 265 270
 Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
 275 280 285
 Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
 290 295 300
 Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln
 305 310 315 320
 Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
 325 330 335
 Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
 340 345 350
 Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
 355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
450 455 460

Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
465 470 475 480

Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
485 490 495

Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
500 505 510

Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
515 520 525

Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
530 535 540

Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
545 550 555 560

Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
565 570 575

Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
580 585 590

Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
595 600 605

Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val
610 615 620

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val
625 630 635 640

Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser
645 650 655

Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys
660 665 670

His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn
675 680 685

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr

690				695				700							
Asp 705	Ile	Thr	Ile	Gln	Gly 710	Gly	Asp	Asp	Val	Phe 715	Lys	Glu	Asn	Tyr	Val 720
Thr	Leu	Gln	Gly	Thr 725	Phe	Asp	Glu	Cys	Tyr 730	Pro	Thr	Tyr	Leu	Tyr 735	Gln
Pro	Ile	Asp	Glu 740	Ser	Lys	Leu	Lys	Ala 745	Tyr	Thr	Arg	Tyr	Gln 750	Leu	Arg
Gly	Tyr	Ile 755	Glu	Asp	Ser	Gln	Asp 760	Leu	Glu	Ile	Tyr	Leu 765	Ile	Arg	Tyr
Asn 770	Ala	Lys	His	Glu	Thr	Val 775	Asn	Val	Pro	Gly	Thr 780	Gly	Ser	Leu	Trp
Pro 785	Leu	Ser	Ala	Pro	Ser 790	Pro	Ile	Gly	Lys	Cys 795	Gly	Glu	Pro	Asn	Arg 800
Cys	Ala	Pro	His	Leu 805	Glu	Trp	Asn	Pro	Asp 810	Leu	Asp	Cys	Ser	Cys 815	Arg
Asp	Gly	Glu	Lys 820	Cys	Ala	His	His	Ser 825	His	His	Phe	Ser	Leu 830	Asp	Ile
Asp	Val	Gly 835	Cys	Thr	Asp	Leu	Asn 840	Glu	Asp	Leu	Gly	Val 845	Trp	Val	Ile
Phe 850	Lys	Ile	Lys	Thr	Gln	Asp 855	Gly	His	Ala	Arg	Leu 860	Gly	Asn	Leu	Glu
Phe 865	Leu	Glu	Glu	Lys	Pro 870	Leu	Val	Gly	Glu	Ala 875	Leu	Ala	Arg	Val	Lys 880
Arg	Ala	Glu	Lys	Lys 885	Trp	Arg	Asp	Lys	Arg 890	Glu	Lys	Leu	Glu	Trp 895	Glu
Thr	Asn	Ile 900	Val	Tyr	Lys	Glu	Ala	Lys 905	Glu	Ser	Val	Asp	Ala 910	Leu	Phe
Val	Asn	Ser 915	Gln	Tyr	Asp	Arg	Leu 920	Gln	Ala	Asp	Thr	Asn 925	Ile	Ala	Met
Ile 930	His	Ala	Ala	Asp	Lys	Arg 935	Val	His	Ser	Ile	Arg 940	Glu	Ala	Tyr	Leu
Pro 945	Glu	Leu	Ser	Val	Ile 950	Pro	Gly	Val	Asn	Ala 955	Ala	Ile	Phe	Glu	Glu 960
Leu	Glu	Gly	Arg	Ile 965	Phe	Thr	Ala	Phe	Ser 970	Leu	Tyr	Asp	Ala	Arg 975	Asn
Val	Ile	Lys	Asn 980	Gly	Asp	Phe	Asn	Asn 985	Gly	Leu	Ser	Cys	Trp 990	Asn	Val
Lys	Gly	His 995	Val	Asp	Val	Glu	Glu 1000	Gln	Asn	Asn	His	Arg 1005	Ser	Val	Leu
Val	Val 1010	Pro	Glu	Trp	Glu	Ala 1015	Glu	Val	Ser	Gln	Glu 1020	Val	Arg	Val	Cys

1200	1205	1210	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 1215 1220 1225			144
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 1230 1235 1240 1245			192
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 1250 1255 1260			240
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1265 1270 1275			288
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 1280 1285 1290			336
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1295 1300 1305			384
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 1310 1315 1320 1325			432
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 1330 1335 1340			480
TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1345 1350 1355			528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1360 1365 1370			576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1375 1380 1385			624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1390 1395 1400 1405			672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1410 1415 1420			720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1425 1430 1435			768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 1440 1445 1450			816

CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 1455 1460 1465	854
GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 1470 1475 1480 1485	912
ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 1490 1495 1500	960
ATC ATG GCC AGC CCC GTC GGC TTC AGC GGC CCC GAG TTC ACC TTC CCC Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 1505 1510 1515	1008
CTG TAC GGC ACC ATG GGC AAC GCT GCA CCT CAG CAG CGC ATC GTG GCA Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 1520 1525 1530	1056
CAG CTG GGC CAG GGA GTG TAC CGC ACC CTG AGC AGC ACC CTG TAC CGT Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 1535 1540 1545	1104
CGA CCT TTC AAC ATC GGC ATC AAC AAC CAG CAG CTG AGC GTG CTG GAC Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 1550 1555 1560 1565	1152
GGC ACC GAG TTC GCC TAC GGC ACC AGC AGC AAC CTG CCC AGC GCC GTG Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 1570 1575 1580	1200
TAC CGC AAG AGC GGC ACC GTG GAC AGC CTG GAC GAG ATC CCC CCT CAG Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 1585 1590 1595	1248
AAC AAC AAC GTG CCA CCT CGA CAG GGC TTC AGC CAC CGT CTG AGC CAC Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 1600 1605 1610	1296
GTG AGC ATG TTC CGC AGT GGC TTC AGC AAC AGC AGC GTG AGC ATC ATC Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile 1615 1620 1625	1344
CGT GCA CCT ATG TTC AGC TGG ATT CAC CGC AGT GCC GAG TTC AAC AAC Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 1630 1635 1640 1645	1392
ATC ATC CCC AGC AGC CAG ATC ACC CAG ATC CCC CTG ACC AAG AGC ACC Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 1650 1655 1660	1440
AAC CTG GGC AGC GGC ACC AGC GTG GTG AAG GGC CCC GGC TTC ACC GGC Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 1665 1670 1675	1488
GGC GAC ATC CTG CGC CGC ACC AGC CCC GGC CAG ATC AGC ACC CTG CGC Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 1680 1685 1690	1536

GTG	AAC	ATC	ACC	GCC	CCC	CTG	AGC	CAG	CGC	TAC	CGC	GTG	CGC	ATC	CGC	1584
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	
	1695					1700					1705					
TAC	GCC	AGC	ACC	ACC	AAC	CTG	CAG	TTC	CAC	ACC	AGC	ATC	GAC	GGC	CGC	1632
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg	
	1710				1715					1720					1725	
CCC	ATC	AAC	CAG	GGC	AAC	TTC	AGC	GCC	ACC	ATG	AGC	AGC	GGC	AGC	AAC	1680
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn	
				1730					1735					1740		
CTG	CAG	AGC	GGC	AGC	TTC	CGC	ACC	GTG	GGC	TTC	ACC	ACC	CCC	TTC	AAC	1728
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn	
			1745					1750					1755			
TTC	AGC	AAC	GGC	AGC	AGC	GTG	TTC	ACC	CTG	AGC	GCC	CAC	GTG	TTC	AAC	1776
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn	
	1760					1765					1770					
AGC	GGC	AAC	GAG	GTG	TAC	ATC	GAC	CGC	ATC	GAG	TTC	GTG	CCC	GCC	GAG	1824
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu	
	1775					1780				1785						
GTG	ACC	TTC	GAG	GCC	GAG	TAC	GAC	CTG	GAG	AGG	GCT	CAG	AAG	GCC	GTG	1872
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	
	1790				1795					1800					1805	
AAC	GAG	CTG	TTC	ACC	AGC	AGC	AAC	CAG	ATC	GGC	CTG	AAG	ACC	GAC	GTG	1920
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	
				1810					1815					1820		
ACC	GAC	TAC	CAC	ATC	GAT	CAA	GTA	TCC	AAT	TTA	GTT	GAG	TGT	TTA	TCT	1968
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser	
			1825				1830					1835				
GAT	GAA	TTT	TGT	CTG	GAT	GAA	AAA	AAA	GAA	TTG	TCC	GAG	AAA	GTC	AAA	2016
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys	
	1840					1845					1850					
CAT	GCG	AAG	CGA	CTT	AGT	GAT	GAG	CGG	AAT	TTA	CTT	CAA	GAT	CCA	AAC	2064
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	
	1855				1860					1865						
TTT	AGA	GGG	ATC	AAT	AGA	CAA	CTA	GAC	CGT	GGC	TGG	AGA	GGA	AGT	ACG	2112
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	
	1870			1875					1880						1885	
GAT	ATT	ACC	ATC	CAA	GGA	GGC	GAT	GAC	GTA	TTC	AAA	GAG	AAT	TAC	GTT	2160
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	
			1890					1895		</						

Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	
1935						1940				1945						
AAT	GCC	AAA	CAC	GAA	ACA	GTA	AAT	GTG	CCA	GGT	ACG	GGT	TCC	TTA	TGG	2352
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp	
1950					1955				1960					1965		
CCG	CTT	TCA	GCC	CCA	AGT	CCA	ATC	GGC	AAG	TGC	GGG	GAG	CCG	AAT	CGA	2400
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg	
				1970				1975					1980			
TGC	GCT	CCG	CAC	CTG	GAG	TGG	AAC	CCG	GAC	CTA	GAC	TGC	AGC	TGC	AGG	2448
Cys	Ala	Pro	His	Leu	Glu	Trp	Asn	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg	
			1985				1990					1995				
GAC	GGG	GAG	AAG	TGC	GCC	CAC	CAC	AGC	CAC	CAC	TTC	AGC	CTG	GAC	ATC	2496
Asp	Gly	Glu	Lys	Cys	Ala	His	His	Ser	His	His	Phe	Ser	Leu	Asp	Ile	
			2000				2005					2010				
GAC	GTG	GGC	TGC	ACC	GAC	CTG	AAC	GAG	GAC	CTG	GGC	GTG	TGG	GTG	ATC	2544
Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Val	Trp	Val	Ile	
			2015				2020				2025					
TTC	AAG	ATC	AAG	ACC	CAG	GAC	GGC	CAC	GCC	CGC	CTG	GGC	AAT	CTA	GAA	2592
Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu	
2030					2035				2040					2045		
TTT	CTC	GAA	GAG	AAA	CCA	TTA	GTA	GGA	GAA	GCA	CTA	GCT	CGT	GTG	AAA	2640
Phe	Leu	Glu	Glu	Lys	Pro	Leu	Val	Gly	Glu	Ala	Leu	Ala	Arg	Val	Lys	
			2050				2055					2060				
AGA	GCG	GAG	AAA	AAA	TGG	AGA	GAC	AAA	CGT	GAA	AAA	TTG	GAA	TGG	GAA	2688
Arg	Ala	Glu	Lys	Lys	Trp	Arg	Asp	Lys	Arg	Glu	Lys	Leu	Glu	Trp	Glu	
			2065				2070					2075				
ACA	AAT	ATT	GTT	TAT	AAA	GAG	GCA	AAA	GAA	TCT	GTA	GAT	GCT	TTA	TTT	2736
Thr	Asn	Ile	Val	Tyr	Lys	Glu	Ala	Lys	Glu	Ser	Val	Asp	Ala	Leu	Phe	
			2080				2085					2090				
GTA	AAC	TCT	CAA	TAT	GAT	AGA	TTA	CAA	GCG	GAT	ACC	AAC	ATC	GCG	ATG	2784
Val	Asn	Ser	Gln	Tyr	Asp	Arg	Leu	Gln	Ala	Asp	Thr	Asn	Ile	Ala	Met	
			2095				2100				2105					
ATT	CAT	GCG	GCA	GAT	AAA	CGC	GTT	CAT	AGC	ATT	CGA	GAA	GCT	TAT	CTG	2832
Ile	His	Ala	Ala	Asp	Lys	Arg	Val	His	Ser	Ile	Arg	Glu	Ala	Tyr	Leu	
2110					2115				2120					2125		
CCT	GAG	CTG	TCT	GTG	ATT	CCG	GGT	GTC	AAT	GCG	GCT	ATT	TTT	GAA	GAA	2880
Pro	Glu	Leu	Ser	Val	Ile	Pro	Gly	Val	Asn	Ala	Ala	Ile	Phe	Glu	Glu	
			2130				2135					2140				
TTA	GAA	GGG	CGT	ATT	TTC	ACT	GCA	TTC	TCC	CTA	TAT	GAT	GCG	AGA	AAT	2928
Leu	Glu	Gly	Arg	Ile	Phe	Thr	Ala	Phe	Ser	Leu	Tyr	Asp	Ala	Arg	Asn	
			2145				2150					2155				
GTC	ATT	AAA	AAT	GGT	GAT	TTT	AAT	AAT	GGC	TTA	TCC	TGC	TGG	AAC	GTG	2976
Val	Ile	Lys	Asn	Gly	Asp	Phe	Asn	Asn	Gly	Leu	Ser	Cys	Trp	Asn	Val	
			2160				2165					2170				
AAA	GGG	CAT	GTA	GAT	GTA	GAA	GAA	CAA	AAC	AAC	CAC	CGT	TCG	GTC	CTT	3024
Lys	Gly	His	Val	Asp	Val	Glu	Glu	Gln	Asn	Asn	His	Arg	Ser	Val	Leu	

2175	2180	2185	
GTT GTT CCG GAA TGG	GAA GCA GAA GTG	TCA CAA GAA GTT CGT GTC TGT	3072
Val Val Pro Glu Trp	Glu Ala Glu Val Ser	Gln Glu Val Arg Val Cys	
2190	2195	2200 2205	
CCG GGT CGT GGC TAT ATC CTT CGT GTC	ACA GCG TAC AAG GAG GGA TAT		3120
Pro Gly Arg Gly Tyr Ile Leu Arg Val	Thr Ala Tyr Lys Glu Gly Tyr		
	2210 2215	2220	
GGA GAA GGT TGC GTA ACC ATT CAT GAG ATC GAG AAC AAT ACA GAC GAA			3168
Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu			
	2225 2230	2235	
CTG AAG TTT AGC AAC TGT GTA GAA GAG GAA GTA TAT CCA AAC AAC ACG			3216
Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr			
	2240 2245	2250	
GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA GAA GAA TAT GAG GGT ACG			3264
Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr			
	2255 2260	2265	
TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA GCC TAT GAA AGC AAT TCT			3312
Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser			
	2270 2275	2280 2285	
TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT GAA GAA AAA GCA TAT ACA			3360
Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr			
	2290 2295	2300	
GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT AAC AGA GGA TAT GGG GAT			3408
Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp			
	2305 2310	2315	
TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA AAA GAA TTA GAG TAC TTC			3456
Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe			
	2320 2325	2330	
CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC GGA GAA ACG GAA GGA ACA			3504
Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr			
	2335 2340	2345	
TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT ATG GAG GAA TAAG			3547
Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu			
	2350 2355	2360	

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Asp	Asn	Asn	Pro	Asn	Ile	Asn	Glu	Cys	Ile	Pro	Tyr	Asn	Cys	Leu
1				5				10						15	

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
20 25 30

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
65 70 75 80

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
115 120 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
165 170 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala

340				345				350							
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg
		355					360					365			
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp
	370					375					380				
Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val
385					390					395					400
Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln
				405					410					415	
Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His
			420					425					430		
Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile
		435					440					445			
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn
	450					455					460				
Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr
465					470					475					480
Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly	Phe	Thr	Gly
				485					490					495	
Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg
			500					505					510		
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg
		515					520					525			
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg
	530					535					540				
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn
545					550					555					560
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn
				565					570					575	
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn
			580					585					590		
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu
		595					600					605			
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val
	610					615					620				
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val
625					630					635					640
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser
				645					650					655	
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys
			660					665					670		

Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu
 995 1000 1005
 Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys
 1010 1015 1020
 Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr
 1025 1030 1035 1040
 Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu
 1045 1050 1055
 Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr
 1060 1065 1070
 Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr
 1075 1080 1085
 Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser
 1090 1095 1100
 Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr
 1105 1110 1115 1120
 Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp
 1125 1130 1135
 Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe
 1140 1145 1150
 Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr
 1155 1160 1165
 Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
 1170 1175 1180

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(1839..2141, 2239..2547, 2641..2718, 2794..2871, 3001..3135, 3236..3370)
- (D) OTHER INFORMATION: /product= "maize TrpA"

/note= "Maize TrpA sequence as disclosed in Figure 24."

(ix) FEATURE:

- (A) NAME/KEY: TATA_signal
- (B) LOCATION: 1594..1599

(ix) FEATURE:

(A) NAME/KEY: CAAT_signal
(B) LOCATION: 1495..1499

(ix) FEATURE:

(A) NAME/KEY: promoter
(B) LOCATION: 39..1838
(D) OTHER INFORMATION: /function= "Promoter sequence used
in pCIB4433"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTCGGAT CCATTAAAGA AGTCTTTGAA CAGATTCTAG AGATCTAGTT TAATGAGCTC	60
CCAAAAGTCT TGAAAAAATT CAGCGGGGAG GCCATTAGGG CAGGGGTACT GTTATGTTTT	120
AAAGAGAACA CCACTTTCTT GATCTCTTCT AAAGAGAAAT GTTTTGTAAG AAGGATCCTG	180
TCCTCCTCAT CCAACCTTTT CATCGGCAAA TTTTTCATAG AGATATTAGA GGCAAGAGAG	240
GGGCCAAAAA GATCCATGTA AATGGAAGTG GCCACCTGGT TGATACCTCC CTCATCTTCA	300
ACAGAAAATC CATTATGAAA AAGTGAATGG ATTTTAAACT CTTCTTTTTC TTCCCTTTTG	360
CAATGAGCTG AAAATATCTG GTATTATTCT CATCACCTC ATTAATGAAT CTGTCCCTAG	420
CAATTTGCTT TCTCTTGATC CCTTCTGCAG CCACCATGTT TCTTAAATTC CACTCCATAT	480
CAAGCTTTTC CAATCTATCA GAATCTGAGA TGGCTGCAAT CTCTCTCATT TTCTCAAGGA	540
TATCGATGTT ATCCATAAGG TATTTCTTGA ACTTCTTATA TTTCCCTTCG ACATTTATAT	600
TCCATCCTTT CAACATTTTT TTGTTCAATC TTTTTTGTTT TTTTCCTTTC CAAACATCGA	660
TACATTTCTT GCTCCTCACA GGTAAGGACG AGCTTTCAAA AAACCTTCTG CTTTAAAGTC	720
AGGTCTGAGC CTCCAGCAAA GCTCACATAT CTAAAGTCCC TCTTCTTAGT TGGGACAGAG	780
TCAGTGCTAA GACACATGGG AACATGACCA GAAAAAAAAA ATCATATTTA GCCCAGAGAC	840
AACAATATTC TTGTACTGCA AGTCTCGTTA TGGGCTAGCA AAGGAATCTA CCCAACTTCT	900
CAAATGTGTT GGGATGTCAA GTATATAGAC TATTCATCAG TTCCAACCTCT ATCAAACCTGT	960
GCAGCTCAAT TATAGAGTTG AATAAAGTGC TCCATCTATT TGTTCTTATC CTCATATTTG	1020
GTAAAGATAT TAAAATCACC TCCCACCAAC ATTTAAAGTG CACCATTTAA AGTGGCTCGC	1080
GAGCACCAAA CCGCTGAAAA CCGGAAATGT TTAGCACGTT GGCAGCGGGA CCCTTTTCTA	1140
TCTCATCGTG TTCTTCGTTG TCCACCACGG CCCACGGGCC AACGCTCCTC CATCCTGTAG	1200
TGTAGAGTAT ATTCCATTTG CGACCGAGCC GAGCATCGAT CCAGCCACAC TGGCCACTGC	1260
CAGCCAGCCA TGTGGCACTC CTACGTATAC TACGTGAGGT GAGATTCACCT CACATGGGAT	1320
GGGACCGAGA TATTTTACTG CTGTGGTTGT GTGAGAGATA ATAAAGCATT TATGACGATT	1380
GCTGAACAGC ACACACCATG CGTCCAGATA GAGAAAGCTT TCTCTCTTTA TTCGCATGCA	1440
TGTTTCATTA TCTTTTATCA TATATATATA ACACATATTA AATGATTCTT CGTTCCAATT	1500

TATAATTCAT	TTGACTTTTT	TATCCACCGA	TGCTCGTTTT	ATTAAAAAAA	ATATTATAAT	1560
TATTGTTACT	TTTTGTTGTA	ATATTGTTTA	GCATATAATA	AACTTTGATA	CTAGTATGTT	1620
TCCGAGCAAA	AAAAAATATT	AATATTTAGA	TTACGAGCCC	ATTAATTAAT	TATATTCGAG	1680
ACAAGCGAAG	CAAAGCAAAG	CAAGCTAATG	TTGCCCCTGC	TGTGCATGCA	GAGGCCCGCT	1740
CTTGCTATAA	ACGAGGCAGC	TAGACGCGAC	TCGACTCATC	AGCCTCATCA	ACCTCGACGA	1800
AGGAGGAACG	AACGGACAGG	TTGTTGCACA	GAAGCGAC	ATG GCT TTC GCG CCC		1855
				Met Ala Phe Ala Pro		
				1	5	
AAA ACG TCC TCC TCC TCC TCG CTG TCC TCG GCG TTG CAG GCA GCT CAG	1901					
Lys Thr Ser Ser Ser Ser Ser Leu Ser Ser Ala Leu Gln Ala Ala Gln						
	10		15		20	
TCG CCG CCG CTG CTC CTG AGG CGG ATG TCG TCG ACC GCA ACA CCG AGA	1949					
Ser Pro Pro Leu Leu Leu Arg Arg Met Ser Ser Thr Ala Thr Pro Arg						
	25		30		35	
CGG AGG TAC GAC GCG GCC GTC GTC GTC ACT ACC ACC ACC ACT GCT AGA	1997					
Arg Arg Tyr Asp Ala Ala Val Val Val Thr Thr Thr Thr Thr Ala Arg						
	40		45		50	
GCT GCG GCG GCT GCT GTC ACG GTT CCC GCC GCC CCG CCG CAG GCG GGC	2045					
Ala Ala Ala Ala Ala Val Thr Val Pro Ala Ala Pro Pro Gln Ala Gly						
	55		60		65	
CGC CGC CGC CGG TGC CAC CAA AGC AAG CGG CGG CAC CCG CAG AGG AGG	2093					
Arg Arg Arg Arg Cys His Gln Ser Lys Arg Arg His Pro Gln Arg Arg						
	70		75		80	85
AGC CGT CCG GTG TCG GAC ACC ATG GCG GCG CTC ATG GCC AAG GGC AAG	2141					
Ser Arg Pro Val Ser Asp Thr Met Ala Ala Leu Met Ala Lys Gly Lys						
	90		95		100	
GTTCGTATAG TACGCGCGCG TGTCGTCGTC GTTATTTTGC GCATAGGCGC GGACATACAC	2201					
GTGCTTTAGC TAGCTAACAG CTAGATCATC GGTGCAG ACG GCG TTC ATC CCG TAC	2256					
				Thr Ala Phe Ile Pro Tyr		
				105		
ATC ACC GCC GGC GAC CCG GAC CTA GCG ACG ACG GCC GAG GCG CTG CGT	2304					
Ile Thr Ala Gly Asp Pro Asp Leu Ala Thr Thr Ala Glu Ala Leu Arg						
	110		115		120	
CTG CTG GAC GGC TGT GGC GCC GAC GTC ATC GAG CTG GGG GTA CCC TGC	2352					
Leu Leu Asp Gly Cys Gly Ala Asp Val Ile Glu Leu Gly Val Pro Cys						
	125		130		135	
TCG GAC CCC TAC ATC GAC GGG CCC ATC ATC CAG GCG TCG GTG GCG CGG	2400					
Ser Asp Pro Tyr Ile Asp Gly Pro Ile Ile Gln Ala Ser Val Ala Arg						
	140		145		150	155
GCT CTG GCC AGC GGC ACC ACC ATG GAC GCC GTG CTG GAG ATG CTG AGG	2448					
Ala Leu Ala Ser Gly Thr Thr Met Asp Ala Val Leu Glu Met Leu Arg						
	160		165		170	

GAG GTG ACG CCG GAG CTG TCG TGC CCC GTG GTG CTC CTC TCC TAC TAC Glu Val Thr Pro Glu Leu Ser Cys Pro Val Val Leu Leu Ser Tyr Tyr 175 180 185	2496
AAG CCC ATC ATG TCT CGC AGC TTG GCC GAG ATG AAA GAG GCG GGG GTC Lys Pro Ile Met Ser Arg Ser Leu Ala Glu Met Lys Glu Ala Gly Val 190 195 200	2544
CAC GGTAAC TATA GCTAGCTCTT CCGATCCCCC TTCAATTAAT TAATTTATAG His	2597
TAGTCCATTC ATGTGATGAT TTTTGTTTTT CTTTTTACTG ACA GGT CTT ATA GTG Gly Leu Ile Val 205	2652
CCT GAT CTC CCG TAC GTG GCC GCG CAC TCG CTG TGG AGT GAA GCC AAG Pro Asp Leu Pro Tyr Val Ala Ala His Ser Leu Trp Ser Glu Ala Lys 210 215 220	2700
AAC AAC AAC CTG GAG CTG GTAGGTTGAA TTAAGTTGAT GCATGTGATG Asn Asn Asn Leu Glu Leu 225 230	2748
ATTTATGTAG CTAGATCGAG CTAGCTATAA TTAGGAGCAT ATCAG GTG CTG CTG Val Leu Leu	2802
ACA ACA CCA GCC ATA CCA GAA GAC AGG ATG AAG GAG ATC ACC AAG GCT Thr Thr Pro Ala Ile Pro Glu Asp Arg Met Lys Glu Ile Thr Lys Ala 235 240 245	2850
TCA GAA GGC TTC GTC TAC CTG GTAGTTATAT GTATATATAG ATGGACGACG Ser Glu Gly Phe Val Tyr Leu 250 255	2901
TAACTCATTC CAGCCCCATG CATATATGGA GGCTTCAATT CTGCAGAGAC GACGAAGACC	2961
ACGACGACGA CTAACACTAG CTAGGGGCGT ACGTTGCAG GTG AGC GTG AAC GGA Val Ser Val Asn Gly 260	3015
GTG ACA GGT CCT CGC GCA AAC GTG AAC CCA CGA GTG GAG TCA CTC ATC Val Thr Gly Pro Arg Ala Asn Val Asn Pro Arg Val Glu Ser Leu Ile 265 270 275	3063
CAG GAG GTT AAG AAG GTG ACT AAC AAG CCC GTT GCT GTT GGC TTC GGC Gln Glu Val Lys Lys Val Thr Asn Lys Pro Val Ala Val Gly Phe Gly 280 285 290	3111
ATA TCC AAG CCC GAG CAC GTG AAG CAGGTACGTA CGTAGCTGAC CAAAAAAAC Ile Ser Lys Pro Glu His Val Lys 295 300	3165
TGTTAACAAG TTTTGTTTGA CAAGCCGGCT ACTAGCTAGC TAACAGTGAT CAGTGACACA	3225
CACACACACA CAG ATT GCG CAG TGG GGC GCT GAC GGG GTG ATC ATC GGC Gln Ile Ala Gln Trp Gly Ala Asp Gly Val Ile Ile Gly 305 310	3274
AGC GCC ATG GTG AGG CAG CTG GGC GAA GCG GCT TCT CCC AAG CAA GGC	3322

Ser	Ala	Met	Val	Arg	Gln	Leu	Gly	Glu	Ala	Ala	Ser	Pro	Lys	Gln	Gly	
315					320					325					330	
CTG	AGG	AGG	CTG	GAG	GAG	TAT	GCC	AGG	GGC	ATG	AAG	AAC	GCG	CTG	CCA	3370
Leu	Arg	Arg	Leu	Glu	Glu	Tyr	Ala	Arg	Gly	Met	Lys	Asn	Ala	Leu	Pro	
			335						340					345		
TGAGTCCATG	ACAAAGTAAA	ACGTACAGAG	ACACTTGATA	ATATCTATCT	ATCATCTCGG											3430
AGAAGACGAC	CGACCAATAA	AAATAAGCCA	AGTGGAAGTG	AAGCTTAGCT	GTATATACAC											3490
CGTACGTCGT	CGTCGTCGTT	CCGGATCGAT	CTCGGCCGGC	TAGCTAGCAG	AACGTGTACG											3550
TAGTAGTATG	TAATGCATGG	AGTGTGGAGC	TACTAGCTAG	CTGGCCGTTT	ATTTCGATTAT											3610
AATTCTTCGC	TCTGCTGTGG	TAGCAGATGT	ACCTAGTCGA	TCTTGTACGA	CGAAGAAGCT											3670
GGCTAGCTAG	CCGTCTCGAT	CGTATATGTA	CTGATTAATC	TGCAGATTGA	ATAAAAACTA											3730
CAGTACGCAT	ATGATGCGTA	CGTACGTGTG	TATAGTTTGT	GCTCATATAT	GCTCCTCATC											3790
ACCTGCCTGA	TCTGCCCATC	GATCTCTCTC	GTACTCCTTC	CTGTTAAATG	CCTTCTTTGA											3850
CAGACACACC	ACCACCAGCA	GCAGTGACGC	TCTGCACGCC	GCCGCTTTAA	GACATGTAAG											3910
ATATTTTAAG	AGGTATAAGA	TACCAAGGAG	CACAAATCTG	GAGCACTGGG	ATATTGCAAA											3970
GACAAAAAAA	AAACAAAATT	AAAGTCCCAC	CAAAGTAGAG	ATAGTAAAGA	GGTGGATGGA											4030
TTAAATTTAT	CTCATGATTT	TTGGATCTGC	TCAAATAGAT	CGATATGGTA	TTCAGATCTA											4090
TGTTGTATAG	CCTTTTCATT	AGCTTTCTGA	AAAAAAATG	GTATGATGAG	TGCGGAGTAG											4150
CTAGGGCTGT	GAAGGAGTCG	GATGGGCTTC	CACGTACTTG	TTTGTGGCCC	TAGTCCGGTT											4210
CTATTTAGGT	CCGATCCGAG	TCCGGCATGG	TCCGGTTCCA	TACGGGCTAG	GACCAAGCTC											4270
GGCACGTGAG	TTTTAGGCCC	GTCGGCTAGC	CCGAGCACGA	CCCCTTTTTT	AACTGGCTAG											4330
GACTCGCCCA	TTTAATAAGA	CAAACATTGC	AAAAAATAGC	TCTATTTTTT	ATTTAAAATA											4390
TATTGTTTAT	TTGTGAAATG	TGTATTATTT	GTAATATATA	TTATTGTATA	TAGTTATATC											4450
TTCAATTATG	ATTTATAAAT	ATGTTTTTTT	TTATGAACTC	AATTTTAAGT	TTGATTTATG											4510
CGTTGGCGGG	CTCGAGGAGG	CACGGTGAAC	ATTTTTGGGT	CGGGCTTAAC	GGGTCGGCCC											4570
GGCCCGGTTT	GGCCCATCCA	CGGCCCATCC	CGTGTCGGCC	TCGTTCGGTG	AGTTCAGCCC											4630
GTCGGACAAC	CCGTCCCCGG	CCCGGATAAT	TAATCGGGCC	TAACCGTGGC	GTGCTTAAAC											4690
GGTCCGTGCC	TCAACGGACC	GGGCCGCGGG	CGGCCCGTTT	GACATCTCTA	GTGGTGTGAT											4750
TAGAGATGGC	GATGGGAACC	GATCACTGAT	TCCGTGTGGA	GAATTCGATA	TCAAGCTTAT											4810
CGATACC																4817

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

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Met Ala Phe Ala Pro Lys Thr Ser Ser Ser Ser Ser Leu Ser Ser Ala
 1           5           10           15
Leu Gln Ala Ala Gln Ser Pro Pro Leu Leu Leu Arg Arg Met Ser Ser
          20           25           30
Thr Ala Thr Pro Arg Arg Arg Tyr Asp Ala Ala Val Val Val Thr Thr
 35           40           45
Thr Thr Thr Ala Arg Ala Ala Ala Ala Val Thr Val Pro Ala Ala
 50           55           60
Pro Pro Gln Ala Gly Arg Arg Arg Arg Cys His Gln Ser Lys Arg Arg
 65           70           75           80
His Pro Gln Arg Arg Ser Arg Pro Val Ser Asp Thr Met Ala Ala Leu
          85           90           95
Met Ala Lys Gly Lys Thr Ala Phe Ile Pro Tyr Ile Thr Ala Gly Asp
          100          105          110
Pro Asp Leu Ala Thr Thr Ala Glu Ala Leu Arg Leu Leu Asp Gly Cys
          115          120          125
Gly Ala Asp Val Ile Glu Leu Gly Val Pro Cys Ser Asp Pro Tyr Ile
          130          135          140
Asp Gly Pro Ile Ile Gln Ala Ser Val Ala Arg Ala Leu Ala Ser Gly
          145          150          155          160
Thr Thr Met Asp Ala Val Leu Glu Met Leu Arg Glu Val Thr Pro Glu
          165          170          175
Leu Ser Cys Pro Val Val Leu Leu Ser Tyr Tyr Lys Pro Ile Met Ser
          180          185          190
Arg Ser Leu Ala Glu Met Lys Glu Ala Gly Val His Gly Leu Ile Val
          195          200          205
Pro Asp Leu Pro Tyr Val Ala Ala His Ser Leu Trp Ser Glu Ala Lys
          210          215          220
Asn Asn Asn Leu Glu Leu Val Leu Leu Thr Thr Pro Ala Ile Pro Glu
          225          230          235          240
Asp Arg Met Lys Glu Ile Thr Lys Ala Ser Glu Gly Phe Val Tyr Leu
          245          250          255
Val Ser Val Asn Gly Val Thr Gly Pro Arg Ala Asn Val Asn Pro Arg
          260          265          270
Val Glu Ser Leu Ile Gln Glu Val Lys Lys Val Thr Asn Lys Pro Val
          275          280          285

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Ala Val Gly Phe Gly Ile Ser Lys Pro Glu His Val Lys Gln Ile Ala
 290 295 300

Gln Trp Gly Ala Asp Gly Val Ile Ile Gly Ser Ala Met Val Arg Gln
 305 310 315 320

Leu Gly Glu Ala Ala Ser Pro Lys Gln Gly Leu Arg Arg Leu Glu Glu
 325 330 335

Tyr Ala Arg Gly Met Lys Asn Ala Leu Pro
 340 345

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..1226
- (D) OTHER INFORMATION: /note= "cDNA sequence for maize pollen-specific calcium dependent protein kinase gene as disclosed in Figure 30."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TG CAG ATC ATG CAC CAC CTC TCC GGC CAG CCC AAC GTG GTG GGC CTC Gln Ile Met His His Leu Ser Gly Gln Pro Asn Val Val Gly Leu 350 355 360	47
CGC GGC GCG TAC GAG GAC AAG CAG AGC GTG CAC CTC GTC ATG GAG CTG Arg Gly Ala Tyr Glu Asp Lys Gln Ser Val His Leu Val Met Glu Leu 365 370 375	95
TGC GCG GGC GGG GAG CTC TTC GAC CGC ATC ATC GCC CGG GGC CAG TAC Cys Ala Gly Gly Glu Leu Phe Asp Arg Ile Ile Ala Arg Gly Gln Tyr 380 385 390	143
ACG GAG CGC GGC GCC GCG GAG CTG CTG CGC GCC ATC GTG CAG ATC GTG Thr Glu Arg Gly Ala Ala Glu Leu Leu Arg Ala Ile Val Gln Ile Val 395 400 405	191
CAC ACC TGC CAC TCC ATG GGG GTG ATG CAC CGG GAC ATC AAG CCC GAG His Thr Cys His Ser Met Gly Val Met His Arg Asp Ile Lys Pro Glu 410 415 420 425	239
AAC TTC CTG CTG CTC AGC AAG GAC GAG GAC GCG CCG CTC AAG GCC ACC Asn Phe Leu Leu Leu Ser Lys Asp Glu Asp Ala Pro Leu Lys Ala Thr 430 435 440	287
GAC TTC GGC CTC TCC GTC TTC TTC AAG GAG GGC GAG CTG CTC AGG GAC	335

Asp	Phe	Gly	Leu	Ser	Val	Phe	Phe	Lys	Glu	Gly	Glu	Leu	Leu	Arg	Asp	
			445					450					455			
ATC	GTC	GGC	AGC	GCC	TAC	TAC	ATC	GCG	CCC	GAG	GTG	CTC	AAG	AGG	AAG	383
Ile	Val	Gly	Ser	Ala	Tyr	Tyr	Ile	Ala	Pro	Glu	Val	Leu	Lys	Arg	Lys	
		460					465					470				
TAC	GGC	CCG	GAG	GCC	GAC	ATC	TGG	AGC	GTC	GGC	GTC	ATG	CTC	TAC	ATC	431
Tyr	Gly	Pro	Glu	Ala	Asp	Ile	Trp	Ser	Val	Gly	Val	Met	Leu	Tyr	Ile	
	475					480					485					
TTC	CTC	GCC	GGC	GTG	CCT	CCC	TTC	TGG	GCA	GAG	AAC	GAG	AAC	GGC	ATC	479
Phe	Leu	Ala	Gly	Val	Pro	Pro	Phe	Trp	Ala	Glu	Asn	Glu	Asn	Gly	Ile	
	490				495					500					505	
TTC	ACC	GCC	ATC	CTG	CGA	GGG	CAG	CTT	GAC	CTC	TCC	AGC	GAG	CCA	TGG	527
Phe	Thr	Ala	Ile	Leu	Arg	Gly	Gln	Leu	Asp	Leu	Ser	Ser	Glu	Pro	Trp	
				510					515					520		
CCA	CAC	ATC	TCG	CCG	GGA	GCC	AAG	GAT	CTC	GTC	AAG	AAG	ATG	CTC	AAC	575
Pro	His	Ile	Ser	Pro	Gly	Ala	Lys	Asp	Leu	Val	Lys	Lys	Met	Leu	Asn	
			525					530					535			
ATC	AAC	CCC	AAG	GAG	CGG	CTC	ACG	GCG	TTC	CAG	GTC	CTC	AAT	CAC	CCA	623
Ile	Asn	Pro	Lys	Glu	Arg	Leu	Thr	Ala	Phe	Gln	Val		Asn	His	Pro	
		540					545					550				
TGG	ATC	AAA	GAA	GAC	GGA	GAC	GCG	CCT	GAC	ACG	CCG	CTT	GAC	AAC	GTT	671
Trp	Ile	Lys	Glu	Asp	Gly	Asp	Ala	Pro	Asp	Thr	Pro	Leu	Asp	Asn	Val	
	555					560					565					
GTT	CTC	GAC	AGG	CTC	AAG	CAG	TTC	AGG	GCC	ATG	AAC	CAG	TTC	AAG	AAA	719
Val	Leu	Asp	Arg	Leu	Lys	Gln	Phe	Arg	Ala	Met	Asn	Gln	Phe	Lys	Lys	
	570				575					580					585	
GCA	GCA	TTG	AGG	ATC	ATA	GCT	GGG	TGC	CTA	TCC	GAA	GAG	GAG	ATC	ACA	767
Ala	Ala	Leu	Arg	Ile	Ile	Ala	Gly	Cys	Leu	Ser	Glu	Glu	Glu	Ile	Thr	
				590					595					600		
GGG	CTG	AAG	GAG	ATG	TTC	AAG	AAC	ATT	GAC	AAG	GAT	AAC	AGC	GGG	ACC	815
Gly	Leu	Lys	Glu	Met	Phe	Lys	Asn	Ile	Asp	Lys	Asp	Asn	Ser	Gly	Thr	
		605						610					615			
ATT	ACC	CTC	GAC	GAG	CTC	AAA	CAC	GGG	TTG	GCA	AAG	CAC	GGG	CCC	AAG	863
Ile	Thr	Leu	Asp	Glu	Leu	Lys	His	Gly	Leu	Ala	Lys	His	Gly	Pro	Lys	
		620					625					630				
CTG	TCA	GAC	AGC	GAA	ATG	GAG	AAA	CTA	ATG	GAA	GCA	GCT	GAC	GCT	GAC	911
Leu	Ser	Asp	Ser	Glu	Met	Glu	Lys	Leu	Met	Glu	Ala	Ala	Asp	Ala	Asp	
		635				640					645					
GGC	AAC	GGG	TTA	ATT	GAC	TAC	GAC	GAA	TTC	GTC	ACC	GCA	ACA	GTG	CAT	959
Gly	Asn	Gly	Leu	Ile	Asp	Tyr	Asp	Glu	Phe	Val	Thr	Ala	Thr	Val	His	
	650				655					660					665	
ATG	AAC	AAA	CTG	GAT	AGA	GAA	GAG	CAC	CTT	TAC	ACA	GCA	TTC	CAG	TAT	1007
Met	Asn	Lys	Leu	Asp	Arg	Glu	Glu	His	Leu	Tyr	Thr	Ala	Phe	Gln	Tyr	
			670					675						680		
TTC	GAC	AAG	GAC	AAC	AGC	GGG	TAC	ATT	ACT	AAA	GAA	GAG	CTT	GAG	CAC	1055
Phe	Asp	Lys	Asp	Asn	Ser	Gly	Tyr	Ile	Thr	Lys	Glu	Glu	Leu	Glu	His	

685	690	695	
GCC TTG AAG GAG CAA GGG TTG TAT GAC GCC GAT AAA ATC AAA GAC ATC			1103
Ala Leu Lys Glu Gln Gly Leu Tyr Asp Ala Asp Lys Ile Lys Asp Ile			
700	705	710	
ATC TCC GAT GCC GAC TCT GAC AAT GAT GGA AGG ATA GAT TAT TCA GAG			1151
Ile Ser Asp Ala Asp Ser Asp Asn Asp Gly Arg Ile Asp Tyr Ser Glu			
715	720	725	
TTT GTG GCG ATG ATG AGG AAA GGG ACG GCT GGT GCC GAG CCA ATG AAC			1199
Phe Val Ala Met Met Arg Lys Gly Thr Ala Gly Ala Glu Pro Met Asn			
730	735	740	745
ATC AAG AAG AGG CGA GAC ATA GTC CTA TAGTGAAGTG AAGCAGCAAG			1246
Ile Lys Lys Arg Arg Asp Ile Val Leu			
750			
TGTGTAATGT AATGTGTATA GCAGCTCAAA CAAGCAAATT TGTACATCTG TACACAAATG			1306
CAATGGGGTT ACTTTTGCAA AAAAAAAAAA AAAAAAAAAA AAA			1349

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gln	Ile	Met	His	His	Leu	Ser	Gly	Gln	Pro	Asn	Val	Val	Gly	Leu	Arg
1				5					10					15	
Gly	Ala	Tyr	Glu	Asp	Lys	Gln	Ser	Val	His	Leu	Val	Met	Glu	Leu	Cys
			20					25					30		
Ala	Gly	Gly	Glu	Leu	Phe	Asp	Arg	Ile	Ile	Ala	Arg	Gly	Gln	Tyr	Thr
			35				40					45			
Glu	Arg	Gly	Ala	Ala	Glu	Leu	Leu	Arg	Ala	Ile	Val	Gln	Ile	Val	His
	50					55					60				
Thr	Cys	His	Ser	Met	Gly	Val	Met	His	Arg	Asp	Ile	Lys	Pro	Glu	Asn
65					70					75				80	
Phe	Leu	Leu	Leu	Ser	Lys	Asp	Glu	Asp	Ala	Pro	Leu	Lys	Ala	Thr	Asp
				85					90					95	
Phe	Gly	Leu	Ser	Val	Phe	Phe	Lys	Glu	Gly	Glu	Leu	Leu	Arg	Asp	Ile
			100					105					110		
Val	Gly	Ser	Ala	Tyr	Tyr	Ile	Ala	Pro	Glu	Val	Leu	Lys	Arg	Lys	Tyr
			115				120					125			
Gly	Pro	Glu	Ala	Asp	Ile	Trp	Ser	Val	Gly	Val	Met	Leu	Tyr	Ile	Phe
	130					135					140				

Leu Ala Gly Val Pro Pro Phe Trp Ala Glu Asn Glu Asn Gly Ile Phe
 145 150 155 160
 Thr Ala Ile Leu Arg Gly Gln Leu Asp Leu Ser Ser Glu Pro Trp Pro
 165 170 175
 His Ile Ser Pro Gly Ala Lys Asp Leu Val Lys Lys Met Leu Asn Ile
 180 185 190
 Asn Pro Lys Glu Arg Leu Thr Ala Phe Gln Val Leu Asn His Pro Trp
 195 200 205
 Ile Lys Glu Asp Gly Asp Ala Pro Asp Thr Pro Leu Asp Asn Val Val
 210 215 220
 Leu Asp Arg Leu Lys Gln Phe Arg Ala Met Asn Gln Phe Lys Lys Ala
 225 230 235 240
 Ala Leu Arg Ile Ile Ala Gly Cys Leu Ser Glu Glu Glu Ile Thr Gly
 245 250 255
 Leu Lys Glu Met Phe Lys Asn Ile Asp Lys Asp Asn Ser Gly Thr Ile
 260 265 270
 Thr Leu Asp Glu Leu Lys His Gly Leu Ala Lys His Gly Pro Lys Leu
 275 280 285
 Ser Asp Ser Glu Met Glu Lys Leu Met Glu Ala Ala Asp Ala Asp Gly
 290 295 300
 Asn Gly Leu Ile Asp Tyr Asp Glu Phe Val Thr Ala Thr Val His Met
 305 310 315 320
 Asn Lys Leu Asp Arg Glu Glu His Leu Tyr Thr Ala Phe Gln Tyr Phe
 325 330 335
 Asp Lys Asp Asn Ser Gly Tyr Ile Thr Lys Glu Glu Leu Glu His Ala
 340 345 350
 Leu Lys Glu Gln Gly Leu Tyr Asp Ala Asp Lys Ile Lys Asp Ile Ile
 355 360 365
 Ser Asp Ala Asp Ser Asp Asn Asp Gly Arg Ile Asp Tyr Ser Glu Phe
 370 375 380
 Val Ala Met Met Arg Lys Gly Thr Ala Gly Ala Glu Pro Met Asn Ile
 385 390 395 400
 Lys Lys Arg Arg Asp Ile Val Leu
 405

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: Protein
(B) LOCATION: 1..464
(D) OTHER INFORMATION: /note= "derived protein sequence of pollen specific CDPK as disclosed in Figure 34."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Val Leu Gly Arg Pro Met Glu Asp Val Arg Ala Thr Tyr Ser Met Gly
1 5 10 15
Lys Glu Leu Gly Arg Gly Gln Phe Gly Val Thr His Leu Cys Thr His
20 25 30
Arg Thr Ser Gly Glu Lys Leu Ala Cys Lys Thr Ile Ala Lys Arg Lys
35 40 45
Leu Ala Ala Arg Glu Asp Val Asp Asp Val Arg Arg Glu Val Gln Ile
50 55 60
Met His His Leu Ser Gly Gln Pro Asn Val Val Gly Leu Arg Gly Ala
65 70 75 80
Tyr Glu Asp Lys Gln Ser Val His Leu Val Met Glu Leu Cys Ala Gly
85 90 95
Gly Glu Leu Phe Asp Arg Ile Ile Ala Arg Gly Gln Tyr Thr Glu Arg
100 105 110
Gly Ala Ala Glu Leu Leu Arg Ala Ile Val Gln Ile Val His Thr Cys
115 120 125
His Ser Met Gly Val Met His Arg Asp Ile Lys Pro Glu Asn Phe Leu
130 135 140
Leu Leu Ser Lys Asp Glu Asp Ala Pro Leu Lys Ala Thr Asp Phe Gly
145 150 155 160
Leu Ser Val Phe Phe Lys Glu Gly Glu Leu Leu Arg Asp Ile Val Gly
165 170 175
Ser Ala Tyr Tyr Ile Ala Pro Glu Val Leu Lys Arg Lys Tyr Gly Pro
180 185 190
Glu Ala Asp Ile Trp Ser Val Gly Val Met Leu Tyr Ile Phe Leu Ala
195 200 205
Gly Val Pro Pro Phe Trp Ala Glu Asn Glu Asn Gly Ile Phe Thr Ala
210 215 220
Ile Leu Arg Gly Gln Leu Asp Leu Ser Ser Glu Pro Trp Pro His Ile
225 230 235 240
Ser Pro Gly Ala Lys Asp Leu Val Lys Lys Met Leu Asn Ile Asn Pro
245 250 255
Lys Glu Arg Leu Thr Ala Phe Gln Val Leu Asn His Pro Trp Ile Lys

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (D) OTHER INFORMATION: /note= "rat protein kinase II protein sequence as shown in Figure 32."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Tyr Gln Leu Phe Glu Glu Leu Gly Lys Gly Ala Phe Ser Val Val Arg
 1 5 10 15
 Arg Cys Val Lys Lys Thr Ser Thr Gln Glu Tyr Ala Ala Lys Ile Ile
 20 25 30
 Asn Thr Lys Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu
 35 40 45
 Ala Arg Ile Cys Arg Leu Leu Lys His Pro Asn Ile Val Arg Leu His
 50 55 60
 Asp Ser Ile Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val
 65 70 75 80
 Thr Gly Gly Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser
 85 90 95
 Glu Ala Asp Ala Ser His Cys Ile His Gln Ile Leu Glu Ser Val Asn
 100 105 110
 His Ile His Gln His Asp Ile Val His Arg Asp Leu Lys Pro Glu Asn
 115 120 125
 Leu Leu Leu Ala Ser Lys Cys Lys Gly Ala Ala Val Lys Leu Ala Asp
 130 135 140
 Phe Gly Leu Ala Ile Glu Val Gln Gly Glu Gln Gln Ala Trp Phe Gly
 145 150 155 160
 Phe Ala Gly Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Asp
 165 170 175
 Pro Tyr Gly Lys Pro Val Asp Ile Trp Ala Cys Gly Val Ile Leu Tyr
 180 185 190
 Ile Leu Leu Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Lys
 195 200 205
 Leu Tyr Gln Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu
 210 215 220
 Trp Asp Thr Val Thr Pro Glu Ala Lys Asn Leu Ile Asn Gln Met Leu
 225 230 235 240
 Thr Ile Asn Pro Ala Lys Arg Ile Thr Ala Asp Gln Ala Leu Lys His
 245 250 255
 Pro Trp Val Cys Gln Arg Ser Thr Val Ala Ser Met Met His Arg Gln
 260 265 270
 Glu Thr Val Glu Cys Leu Arg Lys Phe Asn Ala Arg Arg Lys Leu Lys
 275 280 285
 Gly Ala Ile Leu Thr Thr Met
 290 295

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: Protein
 (B) LOCATION: 1..142
 (D) OTHER INFORMATION: /note= "human calmodulin protein
 sequence as shown in Figure 33."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Leu	Thr	Glu	Glu	Gln	Ile	Ala	Glu	Phe	Lys	Glu	Ala	Phe	Ser	Leu	Phe
1				5					10					15	
Asp	Lys	Asp	Gly	Asp	Gly	Thr	Ile	Thr	Thr	Lys	Glu	Leu	Gly	Thr	Val
			20				25						30		
Met	Arg	Ser	Leu	Gly	Gln	Asn	Pro	Thr	Glu	Ala	Glu	Leu	Gln	Asp	Met
			35				40					45			
Ile	Asn	Glu	Val	Asp	Ala	Asp	Gly	Asn	Gly	Thr	Ile	Asp	Phe	Pro	Glu
	50					55					60				
Phe	Leu	Thr	Met	Met	Ala	Arg	Lys	Met	Lys	Asp	Thr	Asp	Ser	Glu	Glu
65					70					75				80	
Glu	Ile	Arg	Glu	Ala	Phe	Arg	Val	Lys	Asp	Lys	Asp	Gly	Asn	Gly	Tyr
				85				90						95	
Ile	Ser	Ala	Ala	Glu	Leu	Arg	His	Val	Met	Thr	Asn	Leu	Gly	Glu	Lys
			100					105					110		
Leu	Thr	Asp	Glu	Glu	Val	Asp	Glu	Met	Ile	Arg	Glu	Ala	Asp	Ile	Asp
			115				120					125			
Gly	Asp	Gly	Gln	Val	Asn	Tyr	Glu	Glu	Phe	Val	Gln	Met	Met		
	130				135						140				

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 463 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: Protein
 (B) LOCATION: 1..463

(D) OTHER INFORMATION: /note= "protein sequence for soybean CDPK as shown in Figure 34."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Val	Leu	Pro	Gln	Arg	Thr	Gln	Asn	Ile	Arg	Glu	Val	Tyr	Glu	Val	Gly	1	5	10	15
Arg	Lys	Leu	Gly	Gln	Gly	Gln	Phe	Gly	Thr	Thr	Phe	Glu	Cys	Thr	Arg	20	25	30	
Arg	Ala	Ser	Gly	Gly	Lys	Phe	Ala	Cys	Lys	Ser	Ile	Pro	Lys	Arg	Lys	35	40	45	
Leu	Leu	Cys	Lys	Glu	Asp	Tyr	Glu	Asp	Val	Trp	Arg	Glu	Ile	Gln	Ile	50	55	60	
Met	His	His	Leu	Ser	Glu	His	Ala	Asn	Val	Val	Arg	Ile	Glu	Gly	Thr	65	70	75	80
Tyr	Glu	Asp	Ser	Thr	Ala	Val	His	Leu	Val	Met	Glu	Leu	Cys	Glu	Gly	85	90	95	
Gly	Glu	Leu	Phe	Asp	Arg	Ile	Val	Gln	Lys	Gly	His	Tyr	Ser	Glu	Arg	100	105	110	
Gln	Ala	Ala	Arg	Leu	Ile	Lys	Thr	Ile	Val	Glu	Val	Val	Glu	Ala	Cys	115	120	125	
His	Ser	Leu	Gly	Val	Met	His	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Phe	Leu	130	135	140	
Phe	Asp	Thr	Ile	Asp	Glu	Asp	Ala	Lys	Leu	Lys	Ala	Thr	Asp	Phe	Gly	145	150	155	160
Leu	Ser	Val	Phe	Tyr	Lys	Pro	Gly	Glu	Ser	Phe	Cys	Asp	Val	Val	Gly	165	170	175	
Ser	Pro	Tyr	Tyr	Val	Ala	Pro	Glu	Val	Leu	Arg	Lys	Leu	Tyr	Gly	Pro	180	185	190	
Glu	Ser	Asp	Val	Trp	Ser	Ala	Gly	Val	Ile	Leu	Tyr	Ile	Leu	Leu	Ser	195	200	205	
Gly	Val	Pro	Pro	Phe	Trp	Ala	Glu	Ser	Glu	Pro	Gly	Ile	Phe	Arg	Gln	210	215	220	
Ile	Leu	Leu	Gly	Lys	Leu	Asp	Phe	His	Ser	Glu	Pro	Trp	Pro	Ser	Ile	225	230	235	240
Ser	Asp	Ser	Ala	Lys	Asp	Leu	Ile	Arg	Lys	Met	Leu	Asp	Gln	Asn	Pro	245	250	255	
Lys	Thr	Arg	Leu	Thr	Ala	His	Glu	Val	Leu	Arg	His	Pro	Trp	Ile	Val	260	265	270	
Asp	Asp	Asn	Ile	Ala	Pro	Asp	Lys	Pro	Leu	Asp	Ser	Ala	Val	Leu	Ser	275	280	285	
Arg	Leu	Lys	Gln	Phe	Ser	Ala	Met	Asn	Lys	Leu	Lys	Lys	Met	Ala	Leu				

290	295	300
Arg Val Ile Ala Glu	Arg Leu Ser Glu Glu	Glu Ile Gly Gly Leu Lys
305	310	315 320
Glu Leu Phe Lys Met	Ile Asp Thr Asp Asn	Ser Gly Thr Ile Thr Phe
325	330	335
Asp Glu Leu Lys Asp	Gly Leu Lys Arg Val	Gly Ser Glu Leu Met Glu
340	345	350
Ser Glu Ile Lys Asp	Leu Met Asp Ala Ala	Asp Ile Asp Lys Ser Gly
355	360	365
Thr Ile Asp Tyr Gly	Glu Phe Ile Ala Ala	Thr Val His Leu Asn Lys
370	375	380
Leu Glu Arg Glu Glu	Asn Leu Val Ser Ala	Phe Ser Tyr Phe Asp Lys
385	390	395 400
Asp Gly Ser Gly Tyr	Ile Thr Leu Asp Glu	Ile Gln Gln Ala Cys Lys
405	410	415
Asp Phe Gly Leu Asp	Asp Ile His Ile Asp	Asp Met Ile Lys Glu Ile
420	425	430
Asp Gln Asp Asn Asp	Gly Gln Ile Asp Tyr	Gly Glu Phe Ala Ala Met
435	440	445
Met Arg Lys Gly Asn	Gly Gly Ile Gly Arg	Arg Thr Met Arg Lys
450	455	460

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1418..1427
- (D) OTHER INFORMATION: /note= "start of mRNA"

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1481..2366

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 2367..2451

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 2452..2602

(ix) FEATURE:
 (A) NAME/KEY: intron
 (B) LOCATION: 2603..2690

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 2691..2804

(ix) FEATURE:
 (A) NAME/KEY: intron
 (B) LOCATION: 2805..2906

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 2907..3075

(ix) FEATURE:
 (A) NAME/KEY: intron
 (B) LOCATION: 3076..3177

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 3178..3304

(ix) FEATURE:
 (A) NAME/KEY: intron
 (B) LOCATION: 3305..3398

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 3399..3498

(ix) FEATURE:
 (A) NAME/KEY: intron
 (B) LOCATION: 3499..3713

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 3714..3811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTAGTAACAC CTCTCCAATC GCTTGGGTTG GCACATTCTT AGCTTTTATC ACATTTTAAG	60
AAATAGAGTT CACCACCTTC AAAATAATGC CTATACAATG AATGATCGCT TGGATGCAAT	120
ATAGCTAGAT TCAACTAGCT ATATATGGTC AATAGAACCC TGTGAGCACC TCACAAACAC	180
GACTTCAATT TTGAGACCCT AAGCGAGTAA ATGGTTAAAG TCCTCTTATT ATTAGTCTTA	240
GGACTTCTCC TTGCTAAATG CTTGTCAGCG ATCTATATAT CTTCCCCACT GCGGGAGATA	300
CTATATATAG GGCCTTGGAC CTCTAGGGTA TCTCAAAGGC CTAGTCACAA CAATTCTCAA	360
CAGTATTTAA TTTTATACAT GTATGAACAG TGTAGGAATT TGAGTGCCCA ACCCAAGAGT	420
GGGAGGTGTA AATTGGGTAG CTAAACTTAA ATAGGGCTCT TCTTATTTAG GTTTATCTAG	480
TCTCTACTTA GACTAATTCA GAAAGAATTT TACAACCTAT GGTTAATCAT ATCTCTAGTC	540

TAAGCAAATT TAGGAAAGTT AAAAGCACAC AATTAGGCAC ATGTGAAAGA TGTGTATGGT	600
AAGTAAAAGA CTTATAAGGA AAAAGTGGGT GAATCCTCAA GATGTGGTGG TATATCCCAA	660
TGATATTAGA TGCCAGAATA TAGGGGGGAA ATCGATGTAT ACCATCTCTA CCAGGATACC	720
TGTGCGGACT GTGCAACTGA CACATGGACC ATGGTGTCTT CTTAGATTTG GTTATTAGCT	780
AATTGCGCTA CAACTTGTTT AAGGCTAGAC CAAATTAAAA AACTAATATT AAACATAAAA	840
AGTTAGGCAA ACTATAGTAA ATTATGCAGC GATCCAACAA CAAGCCATGT CTCGTGGGTC	900
ATGAGCCACG CGTCGGCCAT ACACCCACAT GATGTTTCCA TACGGATGGT CCTTATGCAA	960
TTTTGTCTGC AAAACACAAG CCTTAATACA GCCACGCGAC AATCATGGAA GTGGTCGTTT	1020
TAGGTCTCTA TCATGAAGTT CAGGGAAAAC GCATCAAATG TAATGCAGAG AAATGGTATT	1080
TCTTCTCTTG TAAATCAGGG AGAGGAGTAC CATCAGTACA GATTCAGAAT CAGAATTCAG	1140
TCTTCCAACG ACAATAATCG CAGCATCTTG TAAAAATTTG CAGAAACTTC TGTTTGA	1200
GTAGCCCTGA CCTTTGCAAA TATTTGAAGT TGTGCCTGCT GACACAACCT CAATCTGGAA	1260
GTGCTGTTGA TCAGTTTTGC CAGAAACAGC AAGCAGCCTA TATATATCTG TCACGAGACA	1320
CCCTGCCGCC CTCTTCTTTC CCGCCATTCC CTCCCTACCC TTCAAATCT AGAAACCTTT	1380
TTTTTTCCTC CCGATACGCC CCTCCATCTC TCGCCGTTCA TGTCCGTGGC TGGCTGCCCT	1440
CCGTGGGAGC AGGCGGCCGC ACTCGTTCCC CGCCGCAGCC ATGGGCCAGT GCTGCTCCAA	1500
GGGCGCCGGA GAGGCCCCGC CACCGAGGCG CCAAACGGCA GGCGCCAAGC CGCGGGCGTC	1560
CGCGAACAAC GCCGACGGAC AACGGGCGTC GTCTTCGTCC GCGGTGGCTG CTGCCGCTGC	1620
TGCTGCCGGT GGTGGTGGCG GCGGCACGAC GAAGCCGGCC TCACCCACCG GCGGCGCCAG	1680
GGCCAGCTCC GGCAGCAAAC CGGCGGCGGC CGTGGGCACG GTGCTGGGCC GGCCCATGGA	1740
GGACGTGCGC GCGACCTACT CGATGGGCAA GGAGCTCGGG CGCGGGCAGT TCGGCGTGAC	1800
GCACCTGTGC ACGCACCGGA CGAGCGGCGA GAAGCTGGCG TGCAAGACGA TCGCAAGCG	1860
GAAGCTGGCG GCCAGGGAGG ACGTGGACGA CGTGCGGCGG GAGGTGCAGA TCATGCACCA	1920
CCTCTCCGGC CAGCCCAACG TGGTGGGCCT CCGCGGCGCG TACGAGGACA AGCAGAGCGT	1980
GCACCTCGTC ATGGAGCTGT GCGCGGGCGG GGAGCTCTTC GACCGCATCA TCGCCCGGGG	2040
CCAGTACACG GAGCGCGGCG CCGCGGAGCT GCTGCGCGCC ATCGTGCAGA TCGTGCACAC	2100
CTGCCACTCC ATGGGGGTGA TGCACCGGGA CATCAAGCCC GAGAACTTCC TGCTGCTCAG	2160
CAAGGACGAG GACGCGCCGC TCAAGGCCAC CGACTTCGGC CTCTCCGTCT TCTTCAAGGA	2220
GGGCGAGCTG CTCAGGGACA TCGTCGGCAG CGCCTACTAC ATCGCGCCCG AGGTGCTCAA	2280
GAGGAAGTAC GGCCCGGAGG CCGACATCTG GAGCGTCGGC GTCATGCTCT ACATCTTCCT	2340

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3543
- (D) OTHER INFORMATION: /product= "Full-length, hybrid maize optimized heat stable cryIA(b)"
/note= "DNA sequence as disclosed in Figure 37 as contained in pCIB5515."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
410 415 420	
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
425 430 435 440	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
445 450 455	
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC	192
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
460 465 470	
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC	240
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile	
475 480 485	
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC	288
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala	
490 495 500	
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG	336
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu	
505 510 515 520	
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG	384
Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu	
525 530 535	
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC	432
Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala	
540 545 550	

ATC	CCC	CTG	TTC	GCC	GTG	CAG	AAC	TAC	CAG	GTG	CCC	CTG	CTG	AGC	GTG	480
Ile	Pro	Leu	Phe	Ala	Val	Gln	Asn	Tyr	Gln	Val	Pro	Leu	Leu	Ser	Val	
		555					560					565				
TAC	GTG	CAG	GCC	GCC	AAC	CTG	CAC	CTG	AGC	GTG	CTG	CGC	GAC	GTC	AGC	528
Tyr	Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Val	Leu	Arg	Asp	Val	Ser	
	570					575					580					
GTG	TTC	GGC	CAG	CGC	TGG	GGC	TTC	GAC	GCC	GCC	ACC	ATC	AAC	AGC	CGC	576
Val	Phe	Gly	Gln	Arg	Trp	Gly	Phe	Asp	Ala	Ala	Thr	Ile	Asn	Ser	Arg	
585					590					595					600	
TAC	AAC	GAC	CTG	ACC	CGC	CTG	ATC	GGC	AAC	TAC	ACC	GAC	CAC	GCC	GTG	624
Tyr	Asn	Asp	Leu	Thr	Arg	Leu	Ile	Gly	Asn	Tyr	Thr	Asp	His	Ala	Val	
			605						610					615		
CGC	TGG	TAC	AAC	ACC	GGC	CTG	GAG	CGC	GTG	TGG	GGT	CCC	GAC	AGC	CGC	672
Arg	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	Val	Trp	Gly	Pro	Asp	Ser	Arg	
			620					625					630			
GAC	TGG	ATC	AGG	TAC	AAC	CAG	TTC	CGC	CGC	GAG	CTG	ACC	CTG	ACC	GTG	720
Asp	Trp	Ile	Arg	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Leu	Thr	Leu	Thr	Val	
		635					640					645				
CTG	GAC	ATC	GTG	AGC	CTG	TTC	CCC	AAC	TAC	GAC	AGC	CGC	ACC	TAC	CCC	768
Leu	Asp	Ile	Val	Ser	Leu	Phe	Pro	Asn	Tyr	Asp	Ser	Arg	Thr	Tyr	Pro	
	650					655					660					
ATC	CGC	ACC	GTG	AGC	CAG	CTG	ACC	CGC	GAG	ATT	TAC	ACC	AAC	CCC	GTG	816
Ile	Arg	Thr	Val	Ser	Gln	Leu	Thr	Arg	Glu	Ile	Tyr	Thr	Asn	Pro	Val	
665					670				675						680	
CTG	GAG	AAC	TTC	GAC	GGC	AGC	TTC	CGC	GGC	AGC	GCC	CAG	GGC	ATC	GAG	864
Leu	Glu	Asn	Phe	Asp	Gly	Ser	Phe	Arg	Gly	Ser	Ala	Gln	Gly	Ile	Glu	
				685					690					695		
GGC	AGC	ATC	CGC	AGC	CCC	CAC	CTG	ATG	GAC	ATC	CTG	AAC	AGC	ATC	ACC	912
Gly	Ser	Ile	Arg	Ser	Pro	His	Leu	Met	Asp	Ile	Leu	Asn	Ser	Ile	Thr	
			700					705					710			
ATC	TAC	ACC	GAC	GCC	CAC	CGC	GGC	GAG	TAC	TAC	TGG	AGC	GGC	CAC	CAG	960
Ile	Tyr	Thr	Asp	Ala	His	Arg	Gly	Glu	Tyr	Tyr	Trp	Ser	Gly	His	Gln	
		715					720					725				
ATC	ATG	GCC	AGC	CCC	GTC	GGC	TTC	AGC	GGC	CCC	GAG	TTC	ACC	TTC	CCC	1008
Ile	Met	Ala	Ser	Pro	Val	Gly	Phe	Ser	Gly	Pro	Glu	Phe	Thr	Phe	Pro	
	730					735					740					
CTG	TAC	GGC	ACC	ATG	GGC	AAC	GCT	GCA	CCT	CAG	CAG	CGC	ATC	GTG	GCA	1056
Leu	Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala	
745					750					755					760	
CAG	CTG	GGC	CAG	GGA	GTG	TAC	CGC	ACC	CTG	AGC	AGC	ACC	CTG	TAC	CGT	1104
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg	
			765					770						775		
CGA	CCT	TTC	AAC	ATC	GGC	ATC	AAC	AAC	CAG	CAG	CTG	AGC	GTG	CTG	GAC	1152
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp	
			780					785					790			

GGC	ACC	GAG	TTC	GCC	TAC	GGC	ACC	AGC	AGC	AAC	CTG	CCC	AGC	GCC	GTG	1200
Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val	
		795					800					805				
TAC	CGC	AAG	AGC	GGC	ACC	GTG	GAC	AGC	CTG	GAC	GAG	ATC	CCC	CCT	CAG	1248
Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln	
	810					815					820					
AAC	AAC	AAC	GTG	CCA	CCT	CGA	CAG	GGC	TTC	AGC	CAC	CGT	CTG	AGC	CAC	1296
Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His	
825					830				835						840	
GTG	AGC	ATG	TTC	CGC	AGT	GGC	TTC	AGC	AAC	AGC	AGC	GTG	AGC	ATC	ATC	1344
Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile	
				845					850					855		
CGT	GCA	CCT	ATG	TTC	AGC	TGG	ATT	CAC	CGC	AGT	GCC	GAG	TTC	AAC	AAC	1392
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn	
			860					865					870			
ATC	ATC	CCC	AGC	AGC	CAG	ATC	ACC	CAG	ATC	CCC	CTG	ACC	AAG	AGC	ACC	1440
Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr	
		875					880					885				
AAC	CTG	GGC	AGC	GGC	ACC	AGC	GTG	GTG	AAG	GGC	CCC	GGC	TTC	ACC	GGC	1488
Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly	Phe	Thr	Gly	
	890					895					900					
GGC	GAC	ATC	CTG	CGC	CGC	ACC	AGC	CCC	GGC	CAG	ATC	AGC	ACC	CTG	CGC	1536
Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg	
905				910						915					920	
GTG	AAC	ATC	ACC	GCC	CCC	CTG	AGC	CAG	CGC	TAC	CGC	GTC	CGC	ATC	CGC	1584
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	
				925					930					935		
TAC	GCC	AGC	ACC	ACC	AAC	CTG	CAG	TTC	CAC	ACC	AGC	ATC	GAC	GGC	CGC	1632
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg	
			940					945					950			
CCC	ATC	AAC	CAG	GGC	AAC	TTC	AGC	GCC	ACC	ATG	AGC	AGC	GGC	AGC	AAC	1680
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn	
		955				960						965				
CTG	CAG	AGC	GGC	AGC	TTC	CGC	ACC	GTG	GGC	TTC	ACC	ACC	CCC	TTC	AAC	1728
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn	
	970					975					980					
TTC	AGC	AAC	GGC	AGC	AGC	GTG	TTC	ACC	CTG	AGC	GCC	CAC	GTG	TTC	AAC	1776
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn	
985					990				995						1000	
AGC	GGC	AAC	GAG	GTG	TAC	ATC	GAC	CGC	ATC	GAG	TTC	GTG	CCC	GCC	GAG	1824
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu	
				1005					1010					1015		
GTG	ACC	TTC	GAG	GCC	GAG	TAC	GAC	CTG	GAG	AGG	GCT	CAG	AAG	GCC	GTG	1872
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	
			1020					1025					1030			
AAC	GAG	CTG	TTC	ACC	AGC	AGC	AAC	CAG	ATC	GGC	CTG	AAG	ACC	GAC	GTG	1920

Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	
		1035						1040					1045			
ACC	GAC	TAC	CAC	ATC	GAT	CAA	GTA	TCC	AAT	TTA	GTT	GAG	TGT	TTA	TCT	1968
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser	
		1050					1055				1060					
GAT	GAA	TTT	TGT	CTG	GAT	GAA	AAA	AAA	GAA	TTG	TCC	GAG	AAA	GTC	AAA	2016
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys	
		1065					1070				1075				1080	
CAT	GCG	AAG	CGA	CTT	AGT	GAT	GAG	CGG	AAT	TTA	CTT	CAA	GAT	CCA	AAC	2064
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	
				1085					1090					1095		
TTT	AGA	GGG	ATC	AAT	AGA	CAA	CTA	GAC	CGT	GGC	TGG	AGA	GGA	AGT	ACG	2112
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	
			1100					1105					1110			
GAT	ATT	ACC	ATC	CAA	GGA	GGC	GAT	GAC	GTA	TTC	AAA	GAG	AAT	TAC	GTT	2160
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	
		1115					1120					1125				
ACG	CTA	TTG	GGT	ACC	TTT	GAT	GAG	TGC	TAT	CCA	ACG	TAT	TTA	TAT	CAA	2208
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	
		1130					1135				1140					
AAA	ATA	GAT	GAG	TCG	AAA	TTA	AAA	GCC	TAT	ACC	CGT	TAC	CAA	TTA	AGA	2256
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg	
		1145				1150				1155					1160	
GGG	TAT	ATC	GAA	GAT	AGT	CAA	GAC	TTA	GAA	ATC	TAT	TTA	ATT	CGC	TAC	2304
Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	
			1165					1170						1175		
AAT	GCC	AAA	CAC	GAA	ACA	GTA	AAT	GTG	CCA	GGT	ACG	GGT	TCC	TTA	TGG	2352
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp	
			1180					1185					1190			
CCG	CTT	TCA	GCC	CCA	AGT	CCA	ATC	GGA	AAA	TGT	GGG	GAG	CCG	AAT	CGA	2400
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg	
		1195					1200					1205				
TGC	GCT	CCG	CAC	CTG	GAG	TGG	AAC	CCG	GAC	CTA	GAC	TGC	AGC	TGC	AGG	2448
Cys	Ala	Pro	His	Leu	Glu	Trp	Asn	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg	
		1210				1215					1220					
GAC	GGG	GAG	AAG	TGC	GCC	CAT	CAT	TCC	CAT	CAT	TTC	TCC	TTG	GAC	ATT	2496
Asp	Gly	Glu	Lys	Cys	Ala	His	His	Ser	His	His	Phe	Ser	Leu	Asp	Ile	
		1225			1230					1235					1240	
GAT	GTT	GGA	TGT	ACA	GAC	TTA	AAT	GAG	GAC	TTA	GGT	GTA	TGG	GTG	ATA	2544
Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Val	Trp	Val	Ile	
			1245					1250						1255		
TTC	AAG	ATT	AAG	ACG	CAA	GAT	GGC	CAT	GCA	AGA	CTA	GGA	AAT	CTA	GAA	2592
Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu	
			1260				1265						1270			
TTT	CTC	GAA	GAG	AAA	CCA	TTA	GTA	GGA	GAA	GCA	CTA	GCT	CGT	GTG	AAA	2640
Phe	Leu	Glu	Glu	Lys	Pro	Leu	Val	Gly	Glu	Ala	Leu	Ala	Arg	Val	Lys	

	1275					1280					1285						
AGA Arg	GCG Ala	GAG Glu	AAA Lys	AAA Lys	TGG Trp	AGA Arg	GAC Asp	AAA Lys	CGT Arg	GAA Glu	AAA Lys	TTG Leu	GAA Glu	TGG Trp	GAA Glu	2688	
	1290					1295					1300						
ACA Thr	AAT Asn	ATT Ile	GTT Val	TAT Tyr	AAA Lys	GAG Glu	GCA Ala	AAA Lys	GAA Glu	TCT Ser	GTA Val	GAT Asp	GCT Ala	TTA Leu	TTT Phe	2736	
	1305					1310					1315					1320	
GTA Val	AAC Asn	TCT Ser	CAA Gln	TAT Tyr	GAT Asp	AGA Arg	TTA Leu	CAA Gln	GCG Ala	GAT Asp	ACC Thr	AAC Asn	ATC Ile	GCG Ala	ATG Met	2784	
	1325					1330					1335						
ATT Ile	CAT His	GCG Ala	GCA Ala	GAT Asp	AAA Lys	CGC Arg	GTT Val	CAT His	AGC Ser	ATT Ile	CGA Arg	GAA Glu	GCT Ala	TAT Tyr	CTG Leu	2832	
	1340					1345					1350						
CCT Pro	GAG Glu	CTG Leu	TCT Ser	GTG Val	ATT Ile	CCG Pro	GGT Gly	GTC Val	AAT Asn	GCG Ala	GCT Ala	ATT Ile	TTT Phe	GAA Glu	GAA Glu	2880	
	1355					1360					1365						
TTA Leu	GAA Glu	GGG Gly	CGT Arg	ATT Ile	TTC Phe	ACT Thr	GCA Ala	TTC Phe	TCC Ser	CTA Leu	TAT Tyr	GAT Asp	GCG Ala	AGA Arg	AAT Asn	2928	
	1370					1375					1380						
GTC Val	ATT Ile	AAA Lys	AAT Asn	GGT Gly	GAT Asp	TTT Phe	AAT Asn	AAT Asn	GGC Gly	TTA Leu	TCC Ser	TGC Cys	TGG Trp	AAC Asn	GTG Val	2976	
	1385					1390					1395					1400	
AAA Lys	GGG Gly	CAT His	GTA Val	GAT Asp	GTA Val	GAA Glu	GAA Glu	CAA Gln	AAC Asn	AAC Asn	CAC His	CGT Arg	TCG Ser	GTC Val	CTT Leu	3024	
	1405					1410					1415						
GTT Val	GTT Val	CCG Pro	GAA Glu	TGG Trp	GAA Glu	GCA Ala	GAA Glu	GTG Val	TCA Ser	CAA Gln	GAA Glu	GTT Val	CGT Arg	GTC Val	TGT Cys	3072	
	1420					1425					1430						
CCG Pro	GGT Gly	CGT Arg	GGC Gly	TAT Tyr	ATC Ile	CTT Leu	CGT Arg	GTC Val	ACA Thr	GCG Ala	TAC Tyr	AAG Lys	GAG Glu	GGA Gly	TAT Tyr	3120	
	1435					1440					1445						
GGA Gly	GAA Glu	GGT Gly	TGC Cys	GTA Val	ACC Thr	ATT Ile	CAT His	GAG Glu	ATC Ile	GAG Glu	AAC Asn	AAT Asn	ACA Thr	GAC Asp	GAA Glu	3168	
	1450					1455					1460						
CTG Leu	AAG Lys	TTT Phe	AGC Ser	AAC Asn	TGT Cys	GTA Val	GAA Glu	GAG Glu	GAA Glu	GTA Val	TAT Tyr	CCA Pro	AAC Asn	AAC Asn	ACG Thr	3216	
	1465					1470					1475					1480	
GTA Val	ACG Thr	TGT Cys	AAT Asn	GAT Asp	TAT Tyr	ACT Thr	GCG Ala	ACT Thr	CAA Gln	GAA Glu	GAA Glu	TAT Tyr	GAG Glu	GGT Gly	ACG Thr	3264	
	1485					1490					1495						
TAC Tyr	ACT Thr	TCT Ser	CGT Arg	AAT Asn	CGA Arg	GGA Gly	TAT Tyr	GAC Asp	GGA Gly	GCC Ala	TAT Tyr	GAA Glu	AGC Ser	AAT Asn	TCT Ser	3312	
	1500					1505					1510						
TCT Ser	GTA Val	CCA Pro	GCT Ala	GAT Asp	TAT Tyr	GCA Ala	TCA Ser	GCC Ala	TAT Tyr	GAA Glu	GAA Glu	AAA Lys	GCA Ala	TAT Tyr	ACA Thr	3360	
	1515					1520					1525						

GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT AAC AGA GGA TAT GGG GAT	3438
Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp	
1530 1535 1540	
TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA AAA GAA TTA GAG TAC TTC	3456
Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe	
1545 1550 1555 1560	
CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC GGA GAA ACG GAA GGA ACA	3504
Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr	
1565 1570 1575	
TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT ATG GAG GAA TAA	3546
Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu	
1580 1585	

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Asp	Asn	Asn	Pro	Asn	Ile	Asn	Glu	Cys	Ile	Pro	Tyr	Asn	Cys	Leu
1				5				10						15	
Ser	Asn	Pro	Glu	Val	Glu	Val	Leu	Gly	Gly	Glu	Arg	Ile	Glu	Thr	Gly
			20					25					30		
Tyr	Thr	Pro	Ile	Asp	Ile	Ser	Leu	Ser	Leu	Thr	Gln	Phe	Leu	Leu	Ser
			35				40					45			
Glu	Phe	Val	Pro	Gly	Ala	Gly	Phe	Val	Leu	Gly	Leu	Val	Asp	Ile	Ile
		50				55					60				
Trp	Gly	Ile	Phe	Gly	Pro	Ser	Gln	Trp	Asp	Ala	Phe	Leu	Val	Gln	Ile
	65				70				75					80	
Glu	Gln	Leu	Ile	Asn	Gln	Arg	Ile	Glu	Glu	Phe	Ala	Arg	Asn	Gln	Ala
				85				90						95	
Ile	Ser	Arg	Leu	Glu	Gly	Leu	Ser	Asn	Leu	Tyr	Gln	Ile	Tyr	Ala	Glu
			100					105					110		
Ser	Phe	Arg	Glu	Trp	Glu	Ala	Asp	Pro	Thr	Asn	Pro	Ala	Leu	Arg	Glu
			115				120					125			
Glu	Met	Arg	Ile	Gln	Phe	Asn	Asp	Met	Asn	Ser	Ala	Leu	Thr	Thr	Ala
			130			135					140				
Ile	Pro	Leu	Phe	Ala	Val	Gln	Asn	Tyr	Gln	Val	Pro	Leu	Leu	Ser	Val
	145				150				155					160	
Tyr	Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Val	Leu	Arg	Asp	Val	Ser
				165				170						175	

Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
 500 505 510
 Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
 515 520 525
 Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
 530 535 540
 Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
 545 550 555 560
 Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
 565 570 575
 Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
 580 585 590
 Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
 595 600 605
 Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val
 610 615 620
 Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val
 625 630 635 640
 Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser
 645 650 655
 Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys
 660 665 670
 His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn
 675 680 685
 Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr
 690 695 700
 Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
 705 710 715 720
 Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
 725 730 735
 Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
 740 745 750
 Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
 755 760 765
 Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
 770 775 780
 Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg
 785 790 795 800
 Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg
 805 810 815
 Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile

820					825					830					
Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Val	Trp	Val	Ile
		835					840					845			
Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu
	850					855					860				
Phe	Leu	Glu	Glu	Lys	Pro	Leu	Val	Gly	Glu	Ala	Leu	Ala	Arg	Val	Lys
	865					870					875				880
Arg	Ala	Glu	Lys	Lys	Trp	Arg	Asp	Lys	Arg	Glu	Lys	Leu	Glu	Trp	Glu
				885					890					895	
Thr	Asn	Ile	Val	Tyr	Lys	Glu	Ala	Lys	Glu	Ser	Val	Asp	Ala	Leu	Phe
			900					905					910		
Val	Asn	Ser	Gln	Tyr	Asp	Arg	Leu	Gln	Ala	Asp	Thr	Asn	Ile	Ala	Met
		915					920					925			
Ile	His	Ala	Ala	Asp	Lys	Arg	Val	His	Ser	Ile	Arg	Glu	Ala	Tyr	Leu
	930					935					940				
Pro	Glu	Leu	Ser	Val	Ile	Pro	Gly	Val	Asn	Ala	Ala	Ile	Phe	Glu	Glu
	945					950					955				960
Leu	Glu	Gly	Arg	Ile	Phe	Thr	Ala	Phe	Ser	Leu	Tyr	Asp	Ala	Arg	Asn
				965					970					975	
Val	Ile	Lys	Asn	Gly	Asp	Phe	Asn	Asn	Gly	Leu	Ser	Cys	Trp	Asn	Val
			980						985				990		
Lys	Gly	His	Val	Asp	Val	Glu	Glu	Gln	Asn	Asn	His	Arg	Ser	Val	Leu
		995					1000					1005			
Val	Val	Pro	Glu	Trp	Glu	Ala	Glu	Val	Ser	Gln	Glu	Val	Arg	Val	Cys
	1010					1015					1020				
Pro	Gly	Arg	Gly	Tyr	Ile	Leu	Arg	Val	Thr	Ala	Tyr	Lys	Glu	Gly	Tyr
	1025					1030					1035				1040
Gly	Glu	Gly	Cys	Val	Thr	Ile	His	Glu	Ile	Glu	Asn	Asn	Thr	Asp	Glu
				1045					1050					1055	
Leu	Lys	Phe	Ser	Asn	Cys	Val	Glu	Glu	Glu	Val	Tyr	Pro	Asn	Asn	Thr
			1060					1065					1070		
Val	Thr	Cys	Asn	Asp	Tyr	Thr	Ala	Thr	Gln	Glu	Glu	Tyr	Glu	Gly	Thr
		1075					1080						1085		
Tyr	Thr	Ser	Arg	Asn	Arg	Gly	Tyr	Asp	Gly	Ala	Tyr	Glu	Ser	Asn	Ser
	1090					1095					1100				
Ser	Val	Pro	Ala	Asp	Tyr	Ala	Ser	Ala	Tyr	Glu	Glu	Lys	Ala	Tyr	Thr
	1105					1110					1115				1120
Asp	Gly	Arg	Arg	Asp	Asn	Pro	Cys	Glu	Ser	Asn	Arg	Gly	Tyr	Gly	Asp
				1125					1130					1135	
Tyr	Thr	Pro	Leu	Pro	Ala	Gly	Tyr	Val	Thr	Lys	Glu	Leu	Glu	Tyr	Phe
			1140					1145					1150		

Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr
 1155 1160 1165

Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
 1170 1175 1180

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE74A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCAGATCTGG ATCCATGCAC GCCGTGAAGG GCCCTTCTAG AAGGCCTATC GATAAAGAGC	60
TCCCCGGGGA TGGATTGCAC GCAGGTTC	88

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE72A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCGTTAACAT GTCGACTCAG AAGAACTCGT CAAGAAGGCG	40
---	----

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer P1(a)"

(iii) HYPOTHETICAL: NO

090344E 1.1001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCGACAAGG ATCCAACAAT GG

22

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P1(b) "

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AATTGTCGAC AAGGATCCAA CAATGG

26

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P2(a) "

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ACACGCTGAC GTCGCGCAGC ACG

23

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P2(b) "

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AGCTACACGC TGACGTCGCG CAG

23

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer A1"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AATTGTCGAC

10

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer A2"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCGTGTAGCT

10

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P3(a)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCTGCGCGAC GTCAGCGTGT TCGG

24

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P3(b)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AATTGCTGCG CGACGTCAGC GTG

23

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P4(a)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GGCGTTGCCC ATGGTGCCGT ACAGG

25

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P4(b)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGCTGGCGTT GCCCATGGTG CCG

23

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer B1"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AATTGCTGCG

10

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer B2"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AACGCCAGCT

10

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P5(a)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTCCCCCTGT ACGGCACCAT GGGCAACGCC GC

32

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P5(b) "

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

AATTGTACGG CACCATGGGC AAC

23

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P6(a) "

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GAAGCCGGGG CCCTTCACCA CGCTGG

26

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P6(b) "

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AGCTGAAGCC GGGGCCCTTC ACC

23

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer C1"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AATTGTACGG

10

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer C2 - first half"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TTCCCCTGTA CGG

13

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer C1 - second half"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGCTTCAGCT

10

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer PEPCivs#9 - forward"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTACAAAAAC CAGCAACTC

19

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer PEPCivs#9 reverse"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTGCACAAAG TGGAGTAGT

19

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer P7(a)"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGGTGAAGGG CCCC GGCTTC ACCGG

25

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer P8(a)"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATCATCGATG AGCTCCTACA CCTGATCGAT GTGGTA

36

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer for fourth quarter - second half"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATCAGGAGCT CATCGATGAT

20

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer for third quarter - first half"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTCCCCCTGT A

11

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer MK23A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGGGCTGCGG ATGCTGCCCT

20

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer MK25A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GAGCTGACCC TGACCGTGCT

20

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer MK26A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CACCTGATGG ACATCCTGAA

20

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "sequence in pCIB3073 prior to deletion"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TATAAGGATC CCGGGGGCAA GATCTGAGAT ATG

33

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer KE134A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CGTGACCGAC TACCACATCG ATCAAGTATC CAATTTAGTT GAGT

44

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer KE135A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACTCAACTAA ATTGGATACT TGATCGATGT GGTAGTCGGT CACG

44

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE136A28"

- (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GCAGATCTGA GCTCTTAGGT ACCCAATAGC GTAACGT

37

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE137A28"

- (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCTGATTATG CATCAGCCTA T

21

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE138A28"

- (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCAGATCTGA GCTCTTATTC CTCCATAAGA AGTAATTC

38

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer MK05A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CAAAGGTACC CAATAGCGTA ACG

23

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer MK35A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AACGAGGTGT ACATCGACCG

20

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "forward primer for pCIB4434"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GCACCGATAT CACCATCCAA GGAGGCGATG ACGTATTCAA AG

42

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "reverse primer for pCIB4434"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AGCGCATCGA TTCGGCTCCC CGCACTTGCC GATTGGACTT GGGGCTGAAA G

51

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer #1"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ATTACGTTAC GCTATTGGGT ACCTTTGATG

30

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer #2"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TCCCCGTCCC TGCAGCTGCA GTCTAGGTCC GGGTTCCACT CCAGGTGCGG AGCGCATCGA

60

TTCGGCTCCC CGCACTTGCC GATTGGACTT GGGGCTGA

98

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer #3"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CAAGTGC GGG GAGCCGAATC GATGCGCTCC GCACCTGGAG TGGAACCCGG ACCTAGACTG

60

CAGCTGCAGG GACGGGGAAA AATGTGCCCA TCATTCCC

98

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer #4"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGGTTTCTCT TCGAGAAATT CTAGATTTC

30

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer used to map transcriptional start site for TrpA gene"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CCGTTTCGTTTC CTCCTTCGTC GAGG

24

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "N-terminal peptide from pollen specific protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Thr	Thr	Pro	Leu	Thr	Phe	Gln	Val	Gly	Lys	Gly	Ser	Lys	Pro	Gly	His
1				5				10						15	
Leu	Ile	Leu	Thr	Pro	Asn	Val	Ala	Thr	Ile						
			20					25							

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "internal peptide of pollen specific protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Lys	Pro	Gly	His	Leu	Ile	Leu	Thr	Pro	Asn	Val	Ala	Thr	Ile	Ser	Asp
1				5				10					15		

Val Val Ile Lys
20

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..16
 - (D) OTHER INFORMATION: /note= "internal peptide from pollen specific protein"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ser	Gly	Gly	Thr	Arg	Ile	Ala	Asp	Asp	Val	Ile	Pro	Ala	Asp	Phe	Lys
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..12
 - (D) OTHER INFORMATION: /note= "internal peptide from pollen specific protein"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Glu	His	Gly	Gly	Asp	Asp	Phe	Ser	Phe	Thr	Leu	Lys
1				5					10		

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..12
- (D) OTHER INFORMATION: /note= "internal peptide from pollen specific protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Glu	Gly	Pro	Thr	Gly	Thr	Trp	Thr	Leu	Asp	Thr	Lys
1				5					10		

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide #51"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AARTCRTCAB CACCRTGYTC

20

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide #58"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CCYTTNCCCA CYTGRAA

17

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide PE51"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TGGCCCATGG CTGCGGCGGG GAACGAGTGC GGC

33

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer #42"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGCGGTCGAC CTGCAGGCAT GCGATCTGCA CCTCCCGCCC

40

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer #43"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ATGGGCAAGG AGCTCGGG

18

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer #SK50"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CCCTCAAAA TCTAGAAACC T

21

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer #SK49"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TAATGTCGAC GAACGCGAG AGATGGA

27

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE99A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TGCGGTTACC GCCGATCACA TG

22

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE97A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GCGGTACCGC GTCGACGCGG ATCCCGCGGC GGAAGCTAA G

41

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE100A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTCGTCGACC GCAACA

16

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE98A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GCGGTACCGC GTTAACGCGG ATCCTGTCCG ACACCGGAC

39

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE104A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GATGTCGTCG ACCGCAACAC

20

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE103A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GCGGTACCGC GGATCCTGTC CGACACCGGA CGGCT

35

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE127"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GCGGATCCGG CTGCGGCGGG GAACGA

26

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE150A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATTTCGCATGC ATGTTTCATT ATC

23

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE151A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GCTGGTACCA CGGATCCGTC GCTTCTGTGC AACAACC

37